### STIC-Biotech/ChemLib

From: Sent:

Rao, Manjunath N.

Thursday, June 28, 2001 7:49 AM STIC-Biotech/ChemLib

To: Subject:

sequence search request for 09/668,788

From: Manjunath N. Rao

Art Unit 1652, Room 10D04

Phone: 306-5681

Date: 6-28-01

Please search the following as soon as possible for application with serial number 09/668,788

SEQ ID NO: 1 and 3 against all commercial nucleic acid databases including issued patents database and pending application database and provide a print of all results.

SEQ ID NO: 2 and 4 against all commercial protein databases including issued patents database and pending application database and provide a print of all results.

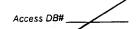
If you have any questions please call me at the above phone number.

### Thanks

Manjunath N. Rao Art Unit 1652 Room CM1, 10D04 Phone 306-5681

MANJUNATH N. RAO, Ph. D Patent Examiner AU 1652, CM1 10D04 703-306-5681

Point of Contact: **Toby Port** Technical Info. Specialist CM1 1E01 TEL: 308-3534 Point of Comact: Toby Port Technical Info. Specialist CM1 1E01 TEL: 308-3534

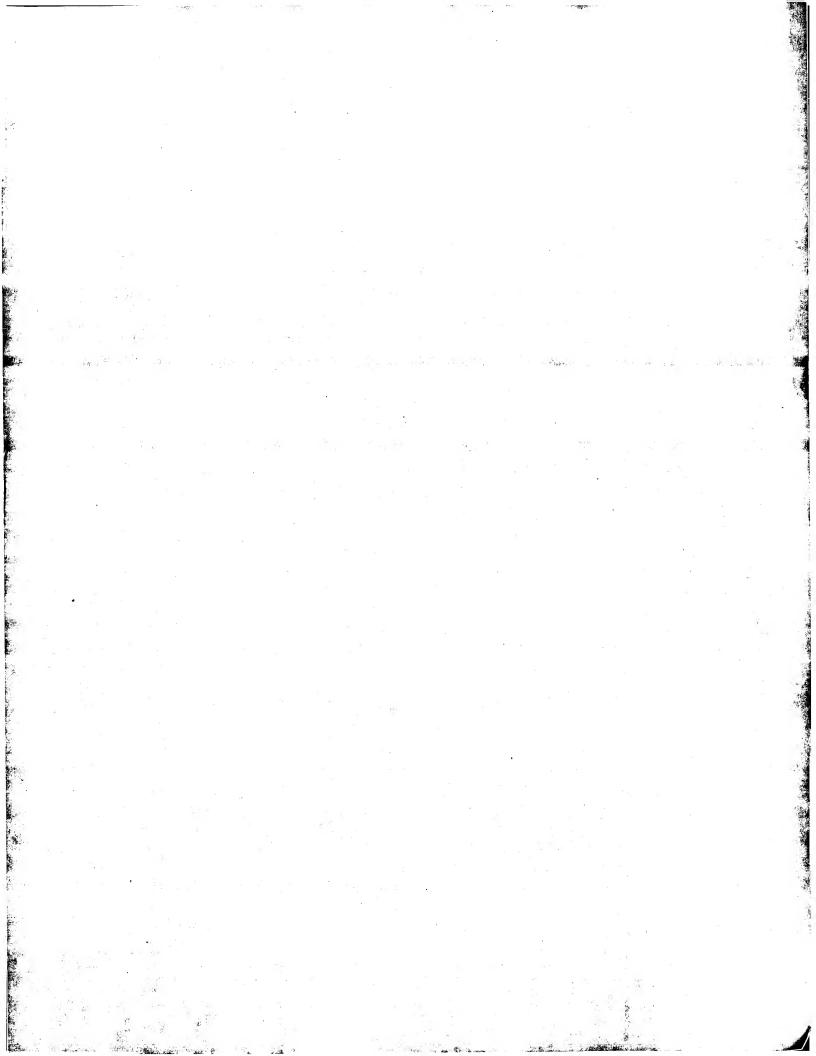


### SEARCH REQUEST FORM

### Scientific and Technical Information Center

Requester's Full Name: Phone Numb	E	xaminer # :	Date:
Art Unit: Phone Numb	er 30	Serial Number:	<del></del>
Mail Box and Bldg/Room Location:	Results	Format Preferred (circle):	PAPER DISK E-MAII
If more than one search is submitted	*******	*****	
Please provide a detailed statement of the search Include the elected species or structures, keywor utility of the invention. Define any terms that in known. Please attach a copy of the cover sheet,	i topic, and describe as rds, synonyms, acronyn nay have a special mear	specifically as possible the sub ns. and registry numbers, and c ting. Give examples or relevan	pect matter to be searched.  ombine with the concept or
Title of Invention:			
Inventors (please provide full names):			
Earliest Priority Filing Date:			
*For Sequence Searches Only* Please include all appropriate serial number.	pertinent information (pa	rent, child, divisional, or issued p	atent numbers) along with the
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PTO-1590 (1-2000)



Run on:

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299115 Bacillus su
AF270166 Staphyloc
AF270394 Staphyloc
X14370 Staphylococ
AX016297 Sequence
AP001513 Bacillus
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53.8 4.7 13408 1 AEO01958 49 4.3 7218 10 166494	11 48 4.2 1266 10 E14811 12 48 4.2 12142 14 CSUG5622 13 44 3.9 150583 88 AC026884 14 44.4 3.9 170934 79 AL354684	44.2 3.8 55593 2 BSAJ2571 44.2 3.8 208230 2 BSUB00008 44.2 3.8 216750 2 BSUB0007 43.2 3.8 1141 10 AXO83744	43.2 3.8 9070 13 AF148842 43 3.7 1569 15 SOL249607 42.8 3.7 2055 12 AB047476 42.6 3.7 158293 85 AC004746	42.6 3.7 172209 75 AC074253 42.2 3.7 5742 96 PYYEL6 42 3.7 137641 78 AF273085 41.8 3.6.104992 60 AC005504	41.8 3.6 150467 87 AC009541 41.8 3.6 169546 60 AC004157 41.8 3.6 172237 88 AC083869 41.6 3.6 187610 67 AC022218	41.4 3.6 5220 2 BBBRGABCD 41.4 3.6 3033 6 CELC18B2 41.4 3.6 52971 1 AE001584 41.4 3.6 157848 65 AC018455	35 41.4 3.6 167032 87 AC012157 36 41.4 3.6 11255 86 AC007912 37 41.2 3.6 138890 86 AC007970 38 41.2 3.6 146000 91 CNSO1RGD	c 39 41.2 3.6 151961 71 AC032443 AC037443 Homo sapi c 40 41.2 3.6 161474 64 AC016198 AC016198 Homo sapi c 41 3.6 48898 70 AC027136 AC027136 Staphyloc c 42 41 3.6 127447 86 AC006344 AC006344 Homo sapi	43 41 3.6 190912 90 AL377559 44 41 3.6 198479 73 AC068483 45 40.8 3.6 140908 74 AC069516	ALIGNMENTS	RESULT 1 XX016296 AX016296 1149 bp DNA PAT 07-SEP-2000 DEFINITION Sequence 1 from Patent W09949052.		_	~	GES F	380 a	100.0%; Score 1149; DB 9; Length 1149; 100.0%; Pred. No. 3.3e-265;	o; aati

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AX016296
LOCUS
DEFINITION
ACCESSION
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SOURCE
ORGANISM

REFERENCE AUTHORS TITLE JOURNAL

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1 waktra,M., Kawata,M., Tsuda,K. and Tanaka,T.
Nucleotide sequence of the thymidylate synthase B and dihydrofolate reductase genes contained in one Bacillus subtilis operon
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3 (bases 1 to 35040)
Capuano, V., Galleron, N., Pujic, P., Sorokin, A.V. and Ehrlich, S.D.
Organization of the Bacillus subtilis chromosome between kdg and
the attachment site of the SPbetta prophage - use of Long Accurate
PCR and yeast artificial chromosomes for sequencing
Unpublished (1996)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ilvD gene; metB gene, naringenin-chalcone synthase; stress-related protein; threonine dehydratase; thyB gene; thymidylate synthase; transport protein; xpt gene; ypad gene; ypbd gene; ypbd gene; yppd gene; yppd
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DNA-binding protein; adenine phosphoribosyltransferase; bcsA gene; basA gene; cold shock protein; cspD gene; degR gene; dfrA gene; dlhydroxfolate reductase; dlhydroxyacid dehydratase; exodeoxyribonuclease; homoserine O-succinyltransferase; ilvA gene;
                                                                                                                                                                                                                                                                                                                         BACYACA 35040 bp DNA BCT 10-APR-1996
Bacillus subtilis (TAC10-9 clone) DNA region between the serA and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sorokin,A.V., Azevedo,V., Zumstein,E., Galleron,N., Ehrlich,S.D.
and Serror,P.
Sequence analysis of the Bacillus subtilis chromosome region between the serA and kdg loci cloned in a yeast artificial
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cerevisiae farnesyl cysteine carboxyl-methyltransferase;
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ive 0; Mismatches 0;
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Pred. No. 5.7e-265;
Mismatches 0;
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/db_xref="G1:2634489"
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/db_xref="G1:2634486"
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/gene="yogC"
/function="unknown"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /gene="yoqB"
complement(4491. .4829)
                                                                                                                                                                                                                                                                 /gene="yoqD"
complement(3281. .4036)
/gene="yoqD"
/function="unknown"
                                                                                                         complement(3063. .3227)
                                                                                                                      /gene="yoqE"
complement(3063. .3227)
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AF270394 3493 bp DNA BCT 01-AUG-2000 Staphylococcus epidermidis strain SR1 clone step.4046a02 genomic sequence.
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1 (bases 1 to 3493)

Kimmerly,W.J., Taylor,J.Davld, Nelsen,A.J., Godlevski,M.M.,
Rubino,M.A., Nelson,F.J., Rivers,P.R., Torruella-Miller,I.
Listenbee,S., Ashanti,C., Altshuller,G., Mamo,L., Shepherd,N.S.,
Fuchs,R., Fleming,T., Guan,X., Du,L., Cain,D.H., Miller,G.S. and
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Taylor, Joavid, Kimmerly, W.J., Nelsen, A.J., Godlevski, M.M.,
Rubino, M.A., Nelson, F.J., Rivers, P.R., Torruella-Miller, I.,
Listenbee, S., Ashanti, C., Altshuller, G., Mamo, L., Shepherd, N.S.,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1118 GGTGGTATCACAATTTCCGAAGGACTTAGTCGTTGTATTCCTATGATTTTTTAAACCCT 1177
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1298 TIAAAGGTIATGTCATCTAAAATGCTAGAATCAAAGGTAGGATATTCTACTAGAAAGATT 1357
      724 gctttaaaaagaatctttgagtgcgcttgaagcggaaaatggtgacaaattaaaagttctg
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           844 ggcggcattactttgacagaagccacagcattggagtgcctgtcattctgtacaaacc
                                                                                                                                                                                     818 AAATTTGAAGAATCTATTGATAAAGAAGAATGGTTATCGCAACAACATTTAGACCCTTCA
                                                                                                                                                                                                                               604 aaaaaagtgcttctgatcatggcaggtgctcacggtgtattaaagaacgtaaaagagctg
                                                                                                                                                                                                                                                                                                                 664 tgcgaaaaccttgtcaaggatgaccaagtgcaagtagttgtcgtgtgcgggaaaaatacg
                                                                                                                                                                                                                                                                                                                                                          938 ATTAATAATATTTTAGAAAAAGTCCAAATTCGCAAGTGGTCATGATTTGTGGACGTAGT
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                                                                                          caatttgaagaatccatgcctgttggcccgatataaaaaagtacaatcttcaccaaac
                                                                   ctgctggagatcggcactcatccaagcaatgtaaaaatcacaggaattccaatcaggccg
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Staphylococcus epidermidis
Bacteria; Firmicutes; Bacillus/Clostridium group;
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AF270394.1
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Taylor, J. David, Kimmerly, W.J., Nelsen, A.J., Godlevski, M.M.,
Rubino, M.A., Nelson, F.J., Rivers, P.R., Torruella-Miller, I.
Listenbee, S., Ashanti, C., Altshuller, G., Mamo, L., Shepherd, N.S.,
Fuchs, R., Fleming, T., Guan, X., Du, L., Cain, D.H., Miller, G.S. and
                                                                                                                                                                                                                          1 (bases 1 to 3118)
Kimmerly, W.J., Taylor, J. David, Nelsen, A.J., Godlevski, M.M.,
Rubino, M.A., Nelson, F.J., Rivers, P.R., Torruella-Miller, I.,
Listenbee, S., Asharit, C., Attshuller, G., Mamo, L., Shepherd, N.S.,
Fuchs, R., Fleming, T., Guan, X., Du, L., Cain, D.H., Miller, G.S. and
                       BCT 01-AUG-2000
SR1 clone step.1051e11 genomic
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Pred. No. 4.3e-22;
0; Mismatches 566; Indels
                                                                                                                                                                Staphylococcus epidermidis
Bacteria; Firmicutes; Bacillus/Clostridium group;
Bacillus/Staphylococcus group; Staphylococcus.
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/strain="SR1"
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                   AF270166 3118 bp DNA
Staphylococcus epidermidis strain
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                                                                                                                                              Staphylococcus epidermidis.
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11.8%;
Best Local Similarity 46.7%;
Matches 510; Conservative
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Furdon, P.J.
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/translation="MMIKQPESKKFFAIISHPDAGKTTLTEKLLYFSGAIREAGTVK
GKLVNLRQYTWMKYEQERGISYTSSYMQEPYDDYEINILDTPGHEDFSEDTYRTLWA
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FRKVSARNVMKQKHFHKGIEQLVQGGAIQXYKTLHTNQIILGAVGGLQFFPFEI

                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Bacteria: Firmicutes; Bacillus/Clostridium group;
Bacillus/Staphylococcus group; Staphylococcus.

1 (bases 1 to 7791)
Ludovice,A.M., Wu,S. and de Lencastre,H.
Molecular cloning and DNA sequencing of the Staphylococcus aureus UDP-N-acetylmuramyl tripeptide synthetase (murE) gene, essential for the optimal expression of methicillin resistance
Microb. Drug Res. 4, 85-90 (1998)
GGTGGTATCACAATTTCCGAAGGACTTAGTCGTTGTATTCCTATGATTTTTTTAAACCCT 1286
                                                                                                                                                                                                 gigaaccgicaigaagaattcicgagicagicacticctictigcagaigaagaiacc 1023
                                                                                                                                                                                                                                   1347 GCAGATACTCCAAATGAGGCAATTGATATTGTTTCTGACTTAACAAATAACGAAGAGACT 1406
                                                                                                                                                                                                                                                                       1024 ttgcatcgcatgaagaaaaacattaaggaccttcatttagcaaactcctcgaagtgatt 1083
                                                                                                                                                                                                                                                                                             Tecnologia
da Quinta
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                                                                                                                                               gtgcctggccaggaaaaagaaaatgcaaacttctttgaagaccgcggagctgccatcgtt
                                                        ggcggcattactttgacagaagccacagccattggagtgcctgtcattctgtacaaaccc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Submitted (30-JUL-1997) A.M. Ludovice, Instituto de Tecn
Qiomica e Biologica, Universidade Nova de Lisbon, R. da
Grande e, Apartado 127, 2780 Oeiras, PORTUGAL
Revised by author 16-JAN-98
Related sequence: L77246.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            murE gene; peptide chain release factor 3; RF3 gene; UDP-N-acetylmuramyl-tripeptide synthetase; ypfP gene
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/codon_start=1
/transl_teable=11
/product="peptide chain rei
/protein_id="CAA74739.1"
/db_xref="GI:3256222"
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Submitted (22-MAY-2000) Departments of Genomic Sciences and
Bioinformatics, Genetics Directorate, Glaxo Wellcome, Inc., 5
Drive, Research Triangle Park, North Carolina 27709-3398, USA
Location/Qualifiers
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       Cain, D.H., Miller, G.S.
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//organism="Staphylococcus epidermidis"
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I (bases I to 975)
Zachringer, U., Heinz, E., Jorasch, P. and Wolter, F. P.
Processive glycosyltransferase
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/translation="MQVRCLKKVKVKRVLGSLEQQIDDITTDSRTAREGSIFVASVGY
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KIKEAVDAGARESHTLEVSSHGLVLGRLRSVEEDVARFSORIDFHGTWEAXGHAK
SLLFSQLGEDLSKEKYVVLNNDDSFSEYLRTVTPYEVFSYGIDEEAQFMAKNIQESLQ
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LEVLDPSLPIDLIDYAHTADGMNKLIDAVQFVKQKLIFLVGMAGERDLTKTPEMGR
VACRADYVIFFPDNADDDFKMLTAAELAKGATHQNYIFLVGMAGERDLTKTPEMGR
VVLASKGREPYQIMPGHIKVPHRDDLIGLEAAXKKFGGGFVD"
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DTWITDILAKSANAQVWALGGKSKELKRSLTAKFKLTRWYLILGTTFHMNEWAASSQL
MITRGGGITITGGRAKCIPWIFLNPAPGGELENAFYPEEKGFGKIADTPEEAIKIVAS
HIGNBEGLTNMISTREGDKIKKYATOTICRDLLDLIGHSSOPQEIYGKVPLYARFFVK"
1452 c 1130 g 2668 t 24 others
EYNVDVVMEPVGRKIAR DIENEDQITDKMNTSRSILVKDRYDDLVFLFENEFATRWF
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EKPDLILLTFPTPVMSVLTEQFNINIPVATVMTDYRLHKNWITPYSTRYYVATKETKQ
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/translation="MVTQNKKILIITGSFGNGHMQVTQSIVNQLNDMNLDHLSVIEHD
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Pred. No. 1.9e-18;
0; Mismatches 486;
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/db_xref="GI:3256223"
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                                                                                                         .3114)
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                                      complement(3009. .3013)
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Patent: WO 9949052-A 2 30-SEP-1999;
FORSCHUNGSZENTRUM BORSTEL (DE); ZAEHRINGER ULRICH (DE); HEINZ ERNST (DE); JORASCH PETRA (DE); WOLTER FRANK P (DE); GVS GES FUER ERWERB UND VERWER (DE)
Location/Qualifiers
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                                                                                                                                                                                      21;
                                                                                                                                                            Length 975;
                                                                                                                                                                                     Indels
                                                                               /organism="Staphylococcus aureus"
/db_xref="taxon:1280"
152 c 169 g 304 t
                                                                                                                                                                                      465;
                                                                                                                                                         Score 118; DB 9;
Pred. No. 5.6e-18;
0; Mismatches 465,
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Best Local Similarity 48.5
Matches 458; Conservative
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1 (sites)
Takami, H., Nakasone, K., Hirama, C., Takaki, Y., Masui, N., Fuji, F.,
Nakamura, Y. and Inoue, A.
An improved physical and genetic map of the genome of alkaliphilic
Bacillus sp. C-125
Extremophiles 3 (1), 21-28 (1999)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          2 (sites).

Takami, H., Nakasone, K., Ogasawara, N., Hirama, C., Nakamura, T.,

Masuli, N., Fuji, F., Takaki, Y., Inoue, A. and Horikoshi, K.

Sequencing of three lambda clones from the genome of alkaliphilic

Bacillus sp. strain C-125

Extremophiles 3 (1), 29-34 (1999)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence analysis of a 32-kb region including the major ribosomal protein gene clusters from alkaliphilic Bacillus sp. strain C-125 Biosci. Biotechnol. Biochem. 63 (2), 452-455 (1999)
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Takami, H., Nakasone, K., Takaki, Y., Maeno, G., Sasaki, R., Masui
Fuji, F., Hirama, C., Nakamura, Y., Ogasawara, N., Kuhara, S. and
Horikoshi, K.
                                                                                                                                                                                                                                                                                                               10-JAN-2001
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Takami,H., Takaki,Y., Nakasone,K., Sakiyama,T., Maeno,G.,
Takami,H., Hirama,C., Fuji,F. and Masui,N.
Genetic analysis of the chromosome of alkaliphilic Bacillus
halodurans C-125
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Takami, H., Masui, N., Nakasone, K. and Horikoshi, K.
Takami, H., Masui, N., Nakasone, K. and Horikoshi, K.
Beplication origin region of the chromosome of alkaliphilic
Bacillus halodurans C-125
Biosci. Biotechnol. Biochem. 63 (6), 1134-1137 (1999)
99356711
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Takami,H., Takaki,Y., Nakasone,K., Hirama,C., Inoue,A. and
Horikoshi,K.
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HORIKOSHI, K. TSUJII;
249-284; Springer-Verlag (1999)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Bacillus halodurans
Bacteria; Firmicutes; Bacillus/Clostridium group;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               943-945 (1999)
                                                                                                                           by DNA BCT genomic DNA, section 7/14.
                                                                                                 cccgtgcctggccaggaaaaagaaaatgcaaacttctttgaaga
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Bacillus/Staphylococcus group; Bacillus
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Biosci. Biotechnol. Biochem. 63,
                                                                                                                                                                                                                                                                                                               AP001513 292550 bp
Bacillus halodurans genc
AP001513 BA000004
AP001513.1 GI:10174345
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Bacillus halodurans DNA.
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Matches 147;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                    Direct Submission
Submitted (22-MAR-2000) Hideto Takami, Japan Marine Science and Technology Center, Deep-sea Microorganisms Research Group; 2-15
Natsushima, Yokosuka, Kanagawa 237-0061, Japan
(E-mail:takamih@jamstec.go.jp,
URL:http://www.jamstec.go.jp/jamstec-e/bio/DEEPSTAR/FResearch.html,
Tel:81-468-67-3895, Fax:81-468-66-6364)
Location/Qualifiers
1. 292550
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SPILNBELAKLKHRKNGFTSTT.63ILFDAKSGAKGLEAALENLESEADOAIEAGKT
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GNKVYPWVAEVRGSTPGVGLISPPPHHDIYSIEDLAELIHDLKNANPQARISVKLVRG
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DESLRRETERKLEAIVNEEGQFFLGMRTVPTDDAMGNARAMPYIDLFIOKSENV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               KAGLDFERKLYVIRKRAENEIGPLVESGSFYFASFSSRTIVYKGMLTTEQVDQFYLDV
VDPDFETALALVHSRFSTNTFPSWERAHPNRYMIHNGEINTVKGNVNWMHAREARFES
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REKAFYGFRSTLMEPMOFPAL VFTDGTOJ GAGLIDROLI, PRESRY YTKDDY I I INASEV
GVLDI DPENVLX KERLHPGHMLLYDLEGGR I I PDDE I KHOI 6.SEHPY EEWV KELLVOL
EDVLET SHVEDT DFGKLRERQLAFGYTY EELITKMI QPMVKEGEDPVGSNGYDSPLAVL
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                                                                                                                                                                                                                        Nakasone, K., Masui, N., Takaki, Y., Sasaki, R., Maeno, G., Sakiyama, T., Hirama, C., Fuji, F. and Takami, H. Characterization and comparative study of the rrn operons of alkaliphilic pacillus halodurans C-125
Takami, H. and Horikoshi, K.
Analysis of the genome of an alkaliphilic Bacillus strain from an
industrial point of view
Extremophiles 4 (2), 99-108 (2000)
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225. 4817
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Takami, H. and Takaki, Y.
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MEDLINE
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AUTHORS
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MEDLINE
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53.3%; Pred. No. 4.1e-06;
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17; Conservative
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4929. .5819
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E Direct Submission

Medical Center Dr, Rockville, MD 20850, USA

Location/Qualifiers

Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /translation-"mttllivglsvllldimilsrpkrppqetqplaprrvRWLDPA
vqavfdrssgkttpvrrgqrvvweprvllkirgdramerlilqqtdlfprasheqll
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Deinococus radiodurans

Bacteria; Thermus/Deinococcus group; Deinococcales; Deinococcus.

Bacteria; Thermus/Deinococcus group; Deinococcales; Deinococcus.

White, O., Eisen, J.A., Heidelberg, J.F., Hickey, E.K., Peterson, J.D., Dodson, R.J., Haft, D.H., Gwinn, M.L., Nelson, W.C., Richardson, D.L., Woffat, K.S., Qin, H., Jiang, L., Pamphile, W., Crosby, M., Shen, M., Vamathevan, J.J., Lam, P., McDonald, L., Utterback, T., Zalewski, C., Makarova, K.S., Aravind, L., Daly, M.J., Fraser, C.M. et, al. Genome sequence of the radioresistant bacterium Deinococcus
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                                                                                                                                                                                                                       Db 253906 CCAATTATCATTCACCAGCCAGTCCTGGTCATGAGGAACACAACCAAAATTTTAATT 253965
                                                                                                                                         Db 253966 GACGCTGCCGCAGCGCTAAGGGTAAAGGGAAGCAAGGAAATTCCTACAACAATCAAGGGA 254025
                                                                                                                                                                                         1003 cttcttgcagatgaagataccttgcatcgcatgaagaaaaacattaaggaccttcattta 1062
cotgicaticigiacaaacccgigcciggccaggaaaaagaaaatgcaaactictigaa 942
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                                                                                               /note="identified by Glimmer2; putative"
/codon_start=1
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/db_xref="G1:6458817"
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/chromosome="1"
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82. //
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/gene="DR1074"
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Deinococcus radiodurans.
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IEGCDWHPESIPDYRERLAALLVPGAVIVLHDAGFGRAYWPLLPSILADLKARGYR
SYLAELGGAARQDMPGLKRRGFLALDAYEDRIGHIHFAGGRADNLFRIARVPFPLEG
ARLAGTFPHGAPALEFHWNHPILVDLGPFASVRQARREDFRVARELJTRPEFADD
GYVFCLSAVSPLLGLLGFENHDLPAADARRILRWANVLRRAYGNDPNAKAPRLSVLTR
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GGIGLGRVTRPAAVVGLLVTALSVMLSLWVAPRANVETRGLYWDALITGAGLSQLVGKT
VDLGOGLTLAAMGYDAGRAROMGVRYPERWDKDNFROGNVYFADAGKFEGNQLSITGYO
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YADAIGADAEGWPELITKLTARGYPGSERDAARVNLNKKLALPFANLVLYLAALPFAL
RFGRTLGVSLGVALVIAVAYYLLFSVGLTLAGLLPGLPEGVWLANIVFALGGLWLLR
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QQAVKQAFABERGVELLGAEHDSVEYLSTFERSFTVDLYEFELRYAPWLYRGFYWLTDQ
DQPWNIISRMFTWLGMGAFKDELRELRPEVVINSFWAPAAVCDTLRAQTGQRFLNCLI
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WIDARAELESBNSLRPGVPLLLLSGGGRGHYAAAADVITELGANGKARVOVIVAPASRQE
GTETIGGATVHHLGFRRDL PRLLAASDLVVORAGGLTVARAPALVITELG
EHNADFLERHGAGLWARARHDVRPLVLRALDPAEHARLSAGARAGIPDAADRVAGAI
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FDDGPDPQTTPAVLAALREADMHATFFVIAGKAQAHPDLIRQMLEEGHEVEAHADKHV
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SGITMSIMTPLLIRDVIKALPHRYPPVLYDRVFSTENGEVHALKNYTINEPFFMGHFP
TEPVMPGYLITEALAQASMFCLHGQMEPGQIGYLAGIEGARFKRKVIPGEQLHLHAKL
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52.00; identified by sequence similarity; putative"
/codon_start=1
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                                                                                                                                                                     /product="(3R)-hydroxymyristoyl-acyl carrier protein
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72.14; identified by sequence similarity; putative"
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/protein_id="AAF10650.1"
/db_xref="G1:6458809"
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1359. .2543
/gene="DR1075"
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/db_xref="G1:6458806"
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/gene="DR1075"
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Unclassified.
1 (bases 1 to 7218)
Dorner.F., Scheiflinger.F. and Falkner.F.Gunter.
Recombinant fowlpox virus
Patent: US 5670367-A 14 23-SEP-1997;
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                        DB 1;
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0.24;
                      Score 53.8; DB 1
Pred. No. 0.018;
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4.3%; Score 49; DB 3
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                      4.78;
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                                                                                                                                                                    /translation="MRAVGLLTLYPCGRGPAEGRGEGGFLGGMLYEWGSKGRLCFDSL
TPYPPPAVYDDLAPIYDQOYDSYRDDIHFYAGLAERAGGRVLEIGAGTGRVTAFLTRR
GANLGVEPSGEMIVGAGARAREGLTLELVQATAGTFSABSERGLIIAPFNALMHLY
TPABQLAALQAIRAHLAPGGGPVFDLYVPHFGAMNTLRHEGETFHYDGSRTDLFLLG
RHDAPRQVITTEXFADTTAPDGALRRAHHTLTQRYTRFEMEWLLRCAGFEAPRVTGS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /translation="MKLTEDGGAHITLDITRDELTVLAGGLLTALDLLTRADAAEDLR
LHLEAEFHGRVGVSRASATALLTELVGIIQAGEDAAQAPLA"
complement(6135. .6794)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /translation="MSAVPTRQOPTVAVVIPARNEEETVGDVVRAALTLTPEVVVASD
SSADATAQVARTAGARVVELLENAGKGPALAALQAPDRETVYMLDGDLGGLTREHLD
VLLRPVLIGELDWIT GIFAGGFASDFGNKWTPQLSQSRACRRDWLLGVPRLAAERWP
EPAITSHLKATDARWAYVELPQVAQVLKETKRGFWSGVKARSKWYGQLLTFWVRRKKD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /product-"light-repressed protein A, putative"
protein_id="AAF10551."
/db_xref="GI:65818"
/translation="MQIYQLSGRNVEVTEPPMREYVEEKLSRLDRYTDQITDARVTLTV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /translation="MKVDRQEQDEARRTRIARAAFELFARTGLDSVSAQDIARAAFVS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RTNLYRYFPSKTHMLLAHFERTVGETRAEALRRLSSGANPQYVWQLYTTRMADIGYRY
RHLAGAVGQAVLGRSRPAEGTPSGPVPQELQTAQTLVSLVEPVLSAMRQQGKLRPDAD
TRFLAALLVDACLMSLLHGGHRNQREVLGDWQDRFSLLMHGALAPNAPALPPDGQRPP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /note="similar to GB:231376 SP:P28368 PID:216333
PID:499384 PID:1762348 percent identity: 67.21; identified
by sequence similarity; putative"
                                                                                                                /product="antibiotic biosynthesis protein LmbJ, putative"
/protein_id="AAF10651.1"
                                  note="similar to GB:X79146 PID:487700 percent identity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /note="similar to SP:P37786 PID:454907 percent identity:
59.86; identified by sequence similarity; putative"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /product="rfbJ protein/conserved hypothetical protein"
/protein_id="AAF10652.1"
/db_xref="G1:6458811"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /product="transcriptional regulator, TetR family"
/protein_id="AAF10653.1"
/db_xref="G1:6458812"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /note="similar to PID:868019 GB:000096 SP:059431
PID:1742672 PID:174580 percent identity: 51.90;
identified by sequence similarity; putative"
/codon.start=1
/transl_table=11
                                                                                                                                                                                                                                                                                                                                                                   /note="identified by Glimmer2; putative" /codon_start=1
                                                                                                                                                                                                                                                                                                                                                                                                                          /product="hypothetical protein"
/protein_id="AAF10659.1"
/db_xref="G1:6458818"
                                                                                                                                                                                                                                                                    FOGGPLVETSEVMVFQARGA"
complement(5801. .6058)
/gene="DR1079"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           complement(6852. 7553)
/gene="DR1081"
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                                                                                                                                                                                                                                                                                                                            complement(5801. 6058)
                                                                                                                                                     /db_xref="GI:6458810"
                                                                                                  /transl_table=11
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                                                                                                                                                                                                                                                                                                                                                    /gene="DR1079"
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/gene="DR1082"
1929. .5819
/qene="DR1078"
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/gene="DR1082"
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CHARGE STATION STORM STATUNGENGS SOBISOLGY FAFS SFELLINDS EGGS SS SH
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SLYLNGFENY GRODG STATION STATIAN STATION STATION STATION STATION STATION STATION STA
                                                                                                                                                                                                                                                                                                                 Direct Submission Submission Submitted (01-JUL-1996) Bioscience & Biotechnology, Tokyo Institute of Technology, Nagatsuta 4259, Midori-Ku, Yokohama 226, Japan Location/Qualifiers
                                                                                                                              cloning of the gene for monogalactosyldiacylglycerol synthase and
Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids
Cucurbitales; Cucurbitaceae; Cucumls.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DNA PRI 10-NOV-2000
10 clone RP11-123G9, complete sequence.
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                                                                                                                                                                                                        2 (bases 1 to 2142)
Ohta,H., Shimojima,M., Iwamatsu,A., Masuda,T., Shioi,Y. and
Takamiya,K.
                                                                            Shioi, Y. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     896 acaaacccgtgcctggccaggaaaaagaaaatgcaaacttctttgaagaccgcggagctg
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /product-"monogalactosyldiacylglycerol synthase"
/protein_id="AAC49624.1"
/db_xref="GI:1805254"
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                                                                                                                        its evolutionary origin
Proc. Natl. Acad. Sci. U.S.A. 94 (1), 333-337 (1997)
97144442
                                                         1 (bases 1 to 2142)
Shimojima,M., Ohta,H., Iwamatsu,A., Masuda,T.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     100;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /db_xref="taxon:3659"
/dev_stage="5-day-old seedlings"
/note="illuminated for 6 h"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /function="glycosyltransferase;
UDP-galactose:1,2-diacylglycerol
3-beta-galactosyltransferase"
                                                                                                                                                                                                                                                                                                                                                                                                                 1. .2142
/organism="Cucumis sativus"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                317. .1894
/EC_number="2.4.1.46"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /strain="Aonagajibai
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Homo sapiens chromosome
AC026884
AC026884.5 GI:11136696
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Best Local Similarity 51.9%;
Matches 108; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /note="i
317. .18
                                                                                                             rakamiya,K.
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Cucumis sativus
Eukaryota, Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           C12N15/09, C07H21/04, C07K14/415, C07K19/00, C12N1/21, C12N9/10, PC
                                                                                                                                                                                                        Eukaryota; Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids I; Cucurbitales; Cucurbitaceee; Cucumis.

1 (bases 1 to 1266)
Ota,H., Shimojima,M., Iwamatsu,A. and Takamiya,K.
Patent: JP 1990101A579-A 2 20-JAN-1998;
KIRIN BREWERY CO LID
                                                                                                                                                                                                                   Spermatophyta;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 959 CAAAGGCGGGCCCTGGAACGATTGCTGAAGCCATGATAAGAGGTCTTCCTATAATTCTGA 1018
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     E14811 1266 bp DNA PAT 28-JUL-1999
CDNA encoding monogalactosyl diacyl glycerol synthase.
E14811
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        acaaacccgtgcctggccaggaaaaagaaaatgcaaacttcttgaagaccgcggagctg
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0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DB 10; Length 1266;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 48; DB 10; I
Pred. No. 0.35;
0; Mismatches 100;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /organism="Cucumis sativus"
/db_xref="taxon:3659"
238 c 319 g 347 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          C12R1:19), (C12N9/10,C12R1:19);
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                                                                                                                                                                                                                                                                                                                                                                                                                              Cucumis sativus
JP 1998014579-A/2
20-JAN-1998
02-JUL-1996 JP 1996172337
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1. .1266
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   strandedness: Double;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         topology: Linear;
hypothetical: No;
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                                                                                                             E14811.1 GI:5709494 JP 1998014579-A/2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                anti-sense: No;
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PC C12N1
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                                                                                                                                                                                                                                                                                  Street, Waltham, MA 02453, USA
On Nov 10, 2000 this sequence version replaced gi:9887582.
Location/Qualifiers
1. 15083
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                                                                                                                        Ulrect Submission
Submitted (25-MAR-2000) Genome Therapeutics Corporation, 100 Beaver
Street, Waltham, MA 02453, USA
Smith,D.R.
Direct Submission
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                                  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 150583)
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 170934)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Homo sapiens chromosome 13 clone RP11-191021, *** SEQUENCING IN PROGRESS ***, 17 unordered pieces.
                                                                                Smith, D.R.
Genome Therapeutics Corporation Sequencing Center: Human Genome
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Submitted (21-JAN-2001) Sanger Centre, Hinxton, Cambridgeshire, CB10 1SA, UK. E-mail enquiries: humquery@sanger.ac.uk Clone requests: clonerequest@sanger.ac.uk
On Aug 21, 2000 this sequence version replaced gi:9213264.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Qy - 154 gaggtaactcaatacctttatttaaaaagcttctcaatcgggaaacagttttatcgtttg 213
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         214 ttttattacggagttgacaaaatctataataacgtaaattcaatatttactttaaaatg 273
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Pred. No. 4.2;
0; Mismatches 56;
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Web site: http://www.sanger.ac.uk
Contact: humquery@sanger.ac.uk
Contact: humquery@sanger.ac.uk
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HTG; HTGS_PHASE1; HTGS_DRAFT.
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AUTHORS
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Assembly program: XGAP4, version 4.5
Sequencing vector: plasmid; L08752; 100% of reads
Chemistry: Dye-terminator Bl4 Dye, 100% of reads
Consensus quality: 160941 bases at least Q40
Consensus quality: 164931 bases at least Q30
Consensus quality: 167496 bases at least Q30
Insert size: 169334; sum-of-contigs
Insert size: 16433; sam-of-contigs
Quality coverage: 3.29% in Q20 bases; sum-of-contigs Quality
coverage: 3.70% in Q20 bases; agarose-fp
                                                                                                                                                                                                                                                                                        NOTE: This is a 'working draft' sequence. It currently consists of 17 contigs. The true order of the pleces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.
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11273 14966: contig of 3694 bp in length
14967 15066: gap of 100 bp
15067 12307: contig of 4241 bp in length
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07: contig of 3423 bp in length
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81123: contig of 7116 bp in length
23: gap of 100 bp
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Monte-"assembly_fragment:01529
fragment_chain:1"
15067. .13907
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ragment_chain:1"
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LEENEMLHYLINKLKTYQYLLKNEPTHYYGSIDAYRESIDKLLKTYADKMUTASL
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                                                                                                                                                                Sequence of the Bacillus subtilis genome between xlyA and ykoR
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Bacillus/Staphylococcus group; Bacillus.
1 (bases 1 to 55593)
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/gene="ykab"
complement(574. .744)
/gene="ykab"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /strain="168
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /gene="xlyA"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /gene~"xlyA"
                                                                                                                                   Devine, K.M.
                                                                                                                                                                                                                 Unpublished
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  154 gaggtaactcaatacctttatttaaaaagcttctcaatcgggaaacagttttatcgtttg 213
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fragment_chain:3"

70485. .73907

/note="sasembly_fragment:00839

fragment_chain:3"

74008 .81123
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a 33064 c 31911 g 50497 t 10
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64987 TTAACTAAAAATT 64974
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Matches 78
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BSAJ2571/C
LOCUS
DEFINITION
ACCESSION
KEYWORDS
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IFKDSNLAKTNKOFRRVQIVTAALQSYTHGTNDAOKAMGIITWALITANLHTSANDIP
TWVQFACATAMGLGTSIGGWKIIKTVGGKIMKIRPVNGVSADLTGAAIIFGATFIHLP
VSTTHVISSSILGVGASHRVKGVNWGTAKRISLHGSSRFRFQRHLVPSPTLF"
                                                                                                                                                                                                                                                                                                                                                                                                                                                      /translation-"MIRRKEDKESLLFEIAKNIDETAEYFVNFKVTNOTTLKEFADT
LKBYETKGDHVHVMIKELMKAFITPIEREDILQLINSLDDVLDGIEHFSAMMEIFSI
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KNLFGNFTDPIKVLOYFEIYETLEEIADSCQSVANNLETIIMKNA"
complement(3506. .4822)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /translation-*MHTEDNGLKERIGLLFALTLVIGTIIGSGVFMKPGAVLAYSGDS
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PILAIAGSFFVLGSTLITDTMSCGLSILIGLAGLPVYYGMKKRKAS
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TDGPGFWVDENLDELGQTIALPPYLEHRRAEIEAKLKPIQ"
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VSLSWPLIVDNIPASKRPYIGSSQTNSVLELAFGYNGIQRLTGQNSGGGQGAPNKDAS
KEMSSSDNTQAPPNQSSSNSSSSDGKSSNGNWAAPPSNGQMPSGGQGGPPSGGDGGQ
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IAGARERRRLSVEQKETVFWVAWLVPIAGFFSVAEFFHHYYLIMLAPRFAPLVGAGWV
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                                                                                                                                                               complement(2613. .3230)
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                                                                                                  complement(2613. .3230)
                                                                                                                                                                                                                             function="unknown"
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/transl_table=
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5211. .6161
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6412. .8562
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gene="ykcB"
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RLMDRKVCDEMKRLKEKNPFVRGLVSWVGSKQTAVEYVRDERLAGETKYPLKKMLKLS
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complement (10063. .11412)
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MIOPKKLYKEGKYYKT-LASGMGRGGNNDIVEWVEKNGKEVASEKWQSSSDQKTENTDS
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PELILEMIEKWKEGYEVVYAVRTKRKGETFFKKQTAAMFYRLLSGMTDIDIPIDTGDF
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SSSSSSAFKSEDSSKISDWVEDLSPAIVGITNLQAQSNSSLFGSSSSDSSEDTESGSG
ALVHLYRNQTGWKAWLLPGAIIATTGFELFILRNYNDQIGVGWSIGVGVIGVLSAIAL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   51772 ATTTTGTTCCGAGCACGGAAGTAAAGAAGCAGCTAATATCAGAGGGTATCGATCAGAACA 51713
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /note="putative serine protease, heat-shock inducible;
homologous to HtrA from E. coli"
/codon_start=1
                                                                                                                                                                                                                /note="putative dolichol phosphate mannose synthetase"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             452 attatgiggcgacagattacgigaaggaaaaactgciggagatcggcactcatccaagca 511
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 55593;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     73; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           51712 ACATATACTTGACCGCATTCCAGTTCACCAAAATTTTGAA 51672
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DB 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 512 atgraaaaatcacaggaattccaatcaggccgcaatttgaa
                                                                                                                                                                                                                                                                                                              /protein_id="CAA05569.1"
/db_xref="GI:2632010"
/db_xref="SWISS-PROT:034319"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    3.8%; Score 44.2; Di
54.7%; Pred. No. 4.3;
iive 0; Mismatches
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Job time: 8429 sec
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                                                                                                                                                                                                                                            /codon_start=1
                                                                                                                                                                                                                                                                                            /product="YkcC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /gene="ykda"
                                                                                                                  8574. .9545
/gene≃"ykcC"
                                                                                                                                                                                       /gene="ykcC"
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88; Conserv
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Matches 88
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GenCore version 4.5
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OM protein . protein search, using sw model

Run on:

June 29, 2001, 08:57:18 ; Search time 28.15 Seconds (without alignments) 1033.701 Million cell updates/sec

Title: Perfect score: Sequence:

US-09-668-788-2 1970 1 MNTHKRVLILTANYGNGHVO......BDIIKESEMMTAKQKAKVLS 382

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

219241 seqs, 76174552 residues Searched:

Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database :

PIR\_68:\* 1: pirl:\* 2: pir2:\* 3: pir3:\* 4: pir4:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result	•				
Score	- :	Match Length	<b>8</b>	di .	Description
1 19:	_	38	7	C69935	cell wall synthesi
3(			ď	E83894	hypothetical prote
3,	353 17.9	411	~	F75439	probable cell wall
			~	C84499	probable monogalac
	60		7	B69860	
6 303,	2		7	T10478	probable 1,2-diacy
30	r.		ď	T05092	
	93		~	T52269	1,2-diacylqlycerol
9			7	JC1275	phospho-N-acetylmu
	195 9.9		7	C70401	phospho-N-acetylmu
			7	E83970	UDP-N-acetylqlucos
	71		7	D64185	UDP-N-acetyldlucos
17	0.5 8.7	363	7	F70195	UDP-N-acetylglucos
			N	E70156	lipopolysaccharide
	69		7	E86823	peptidoglycan synt
15	٥.		7	F64456	hypothetical prote
			7	A72304	UDP-N-acetylglucos
137	2.		7	T34954	probable UDP-N-ace
9 136	.5 6.		~	C71420	hypothetical prote
	<u>.</u>		7	C64664	transferase, pepti
			7	E64432	spore coat polysac
2	34 6.		~	G71852	udp-n-acetyldlucos
. 130	.5 6.		П	C69851	macrolide glycosyl
4 12	.5		7	E70579	probable murg prot
			~	C72340	probable hexosyltr
123	ė.		7	D82763	UDP-N-acetylglucos
_	ė		٦	BVECMG	UDP-N-acetylglucos
8	23	355	7	F85491	hypothetical prote
9 122.	٦.	339	7	B72402	UDP-N-acetylglucos

probable UDP-N-ace	murg protein (murg	UDP-N-acetylqlucos	UTP-qlucose glucos	UDP-N-acetylglucos	probable hexosyltr	capm protein (capM	probable hexosyltr	probable hexosyltr	LPS biosynthesis p	hypothetical prote	UDP-N-acetylqlucos	probable hexosyltr	hypothetical prote	hypothetical prote	sucrose-phosphate
D81306	C71699	G75496	T08395	D70049	F69142	E71699	D70351	C72590	E86651	B64469	B86783	S77553	D84955	S76863	JQ1329
~	7	7	7	7	Н	7	Н	Н	7	7	~	Н	7	7	Н
342	385	418	478	380	400	338	366	363	379	571	362	404	354	371	1068
6.2	6.2	0.9	0.9	0.9	5.9	5.9	5.9	5.9	5.9	5.9	5.8	5.8	5.8	5.7	5.7
122.5	121.5	119	119	.117.5	1117	116.5	116.5	116	116	115.5	114.5	114.5	113.5	113	112.5
30	31	32	33	34	35	36	37	38	39	40	41	42	43	44	45

# ALIGNMENTS

RESULT C6993LF C6993LF C7, Spec C7, Acce C7, Acce R7, Kunh R7, Eh	TESULT 1  C69955  cell wall synthesis homolog ypfP - Bacillus subtilis  c; pecies; Bacillus subtilis  R; Riunst, E; Ogasavara, N; Bascer, I; Albertin, A.M.; Alloni, G; Azevedo, V.; Ber  R; Runst, E; Ogasavara, N; Buscer, I; Fujita, M.; Fujita, Y.; Fuma, S; Galizzi, A.; Gal  1cch, J; Harwood, C.R.; Henaut, A.; Hibert, H.; Holsappel, S; Hosono, S; Hullo, M.  Nature 1300, 249-256, 1997  Nature 1300, 249-256, 1997  N; Authors: Foulger, D; Fritz, C.; Fujita, M.; Fujita, Y.; Fuma, S.; Galizzi, A.; Gal  N; Authors: Lauber, J; Lazarevic, V; Lee, S.M.; Levine, A.; Liu, H.; Masuda, S.; Man  N; Authors: Lauber, J; Lazarevic, V; Lee, S.M.; Levine, A.; Liu, H.; Masuda, S.; Man  N; Authors: Lauber, J; Lazarevic, V; Lee, S.M.; Levine, A.; Landino  N; M.; Ogawa, K.; Ogiwara, A.; Yanaka, E.; Rose, M.; Sadaie, Y.; Scato, T.; Scan  N; Authors: Schleioh, S.; Schroeter, R.; Scoffone, E.; Sekiguchi, J.; Sekowska, A.; Scakeuchi, M.; Tamaka, H.F.; Zumstein, E.; Yoshikawa, H.; Danchin, A.; Yata, K.; Yasumoto, H.; Yamane, R.;  N; Reference number: A65980; MUD:98044033  N; Mctecule type: DNA  N; Reference number: A6580; MUD:98044033  N; Mctecule type: DNA  N; Reference: Strain 168  N; Mctecule type: DNA  N; Residues: 1.382 < KUN>  N; Mctecule type: Mctecule caid sequence not shown; translation not shown  N; Experimental source: Strain 168  C; Scherics: Poly Planting Subtilis  N; Rycos reference: Strain 168  C; Scherics: Rose, M.; Planting Planting Subtilis  N; Rycos reference: Strain 168  C; Scherics: Rose Rose Rose Rose Rose Rose Rose Rose
O O Ma	Query Match 100.0%; Score 1970; DB 2; Length 382; Best Local Similarity 100.0%; Pred. No. 2.4e-127; Matches 382; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy	1 MNTNKRVLILTANYGNGHVQVAKTLYEQCVRLGFQHVTVSNLYQESNPIVSEVTQYLYLK 60 
Qy	61 SFSIGKQFYRLFYYGUDKIYNKRKFNIYFKMGNKRLGELVDEHQPDIIINTFPMIVVPEY 120 
Qy	121: RRRTGRVIPTFNVMTDFCLHKIMVHENVDKXYVATDYVKEKLLEIGTHPSNVKITGIPIR 180 
QY	181 POFEESÄPVGPIYKKYNLSPNKKVLLIMAGAHGVLKNVKELCENLYKDDOVQVVVVCGKN 240 

11;

Gaps

44;

222

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M.; Shen, M.; Vamathevan, J.J.; Lam, P.; McDonald, L.; Utterback, T.; Zalewski, C.; S.; Smith, H.O.; Venter, J.C.; Fraser, C.M. Science 286, 1571-1577, 1999.
A.71tle: Genome sequence of the radioresistant bacterium Deinococcus radiodurans Rl. A;Reference number: A75439
A.Accession: F75439
A.Accession: F75
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               probable monogalactosyldiacylglycerol synthase [imported] - Arabidopsis thaliana C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 02-Feb-2001 #sequence_revision 02-Feb-2001 #text_change 02-Feb-2001
C;Accession: C84499
R;Lin, X; Kaul, S; Rounsley, S.D.; Shea, T.P.; Benito, M.I.; Town, C.D.; Fujii, C.Y.M.; Koo, H.; Moffat, K.S.; Cronin, L.A.; Shen, M.; VanAken, S.E.; Umayam, L.; Tallon, euss, D.; Nierman, W.C.; White, O.; Eisen, J.A.; Salzberg, S.L.; Fraser, C.M.; Venter Nature 402, 761-768, 1999
A;Title: Sequence and analysis of chromosome 2 of the plant Arabidopsis thaliana. A;Recession: C84499
A;Status: preliminary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GB:AE002093; NID:94734000; PIDN:AAD28678.1; GSPDB:GN00139
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           64 I------GKQFYRLFYYGVDKIYNKRKFNIYFKM----GNKRLGELVDEHQPDIIIN 110
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 111 TF--PMIVVPEYRRRGRVIPTFNVMIDFCLHKIWVHENVDKYYVATDYVKEKLLEIGTH 168
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GGITLIEATAIGVPVILYKPVPGQEKENANFFEDRGAAIVVNRHEEILESVTSLLADEDT 341
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 29 RALFMSVSLGAGHDQA-----QQAVKQAFAERGVELLGAEHDSV-----EYLSTFERSFT 78
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RVLILTANYGNGHVQVAKTLYEQCVRLGFQHVTVSNLYQESNPIVSEVTQYL--YLKSFS 63
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TELGNLGRAVQVLVPASRQGEGTETI-----GGATVHLGFRRDLPRLLAASDLVVGKA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          223 ENLVK-DDQVQVVVVCGKNTALKESLSALEAENGDKLKVLGYVERIDELFRITDCMITKP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PSNVKITGIPIRPQFEESMPV-----GPIYKKYNLSPNKKVLLIMAGAHGVLKNVKELC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 411;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 464;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           164; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      17.9%; Score 353; DB 2; 26.2%; Pred. No. 8.7e-17; Live 77; Mismatches 164
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 317; DB 2;
Pred. No. 3e-14;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        342 LHRMKKNIKDLHLANSSEVILEDILK 367
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    16.1%;
25.6%;
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A; Residues: 1-464 <STO>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A;Gene: At2g11810
A;Map position: 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               101;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local S.
Matches 101
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A;Residues: 1-374 <STO>
A;Cross-references: GB:AP001513; GB:BA000004; NID:g10174345; PIDN:BAB05676.1; GSPDB:GN00
A;Experimental source: strain C-125
C;Genetics:
A;Gene: BH1957
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             R;Takami, H.; Nakasone, K.; Takaki, Y.; Maeno, G.; Sasaki, R.; Masui, N.; Fuji, F.; Hirz Nucleic Acids Res. 28, 4317-4331, 2000
A;Title: Complete genome sequence of the alkaliphilic bacterium Bacillus halodurans and A;Accession: B83894
A;Accession: B83894
A;Accession: preliminary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     probable cell wall synthesis protein - Deinococcus radiodurans (strain R1) (Species: Deinococcus radiodurans C; Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 31-Mar-2000 (S, Accession: F75439 R; White; 0.; Eisen, J.A.; Heidelberg, J.F.; Hickey, E.K.; Peterson, J.D.; Dodson, R.J.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         13;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            hypothetical protein BH1957 [imported] - Bacillus halodurans (strain C-125) C;Species: Bacillus halodurans (parter of parter) C;Becies: Bacillus halodurans (parter of parter) C;Becies: Bacillus halodurans (parter of parter) C;Becession: Bassague (parter of parter of
        TALKESLSALEAENGDKLKVLGYVERIDELFRITDCMITKPGGITLTEATAIGVPVILYK 300
                                                PVPGQEKENANFFEDRGAAIVVNRHEEILESVTSLLADEDTLHRMKKNIKDLHLANSSEV 360
                                                                                                                                                                                                   174 ITGIPIRPQFEE-SMPVGPIYKKYNLSPNKKVLLIMAGAHGVLKNVKELCENL-VKDDQV 231
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       125 GRV--IPTFNVMTDFCLHKIWVHENVDKYYVA----TDYVKEKLLEIGTHPSNVK----
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                                                                                                                                                                                                                                                                                                            349 LKKPNAANEIVEQMLLLVKEQQ 370
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Best Local Similarity 27.09
Matches 103; Conservative
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probable 1,2-diacylglycerol 3-beta-galactosyltransferase (EC 2.4.1.46) precursor, chl N.Alternate names: monogalactosyldiacylglycerol synthase (5.5pecles: Cucumis sativus (cucumber) (5.5pecles: Cucumis sativus (cucumber) (5.5pecles: 16-Jul-1999 #sequence_revision 16-Jul-1999 #text_change 21-Jul-2000 (5.5necssion: T10478 #sequence_revision 16-Jul-1999 #text_change 21-Jul-2000 (7.5nimojima, M.; Ohta, H.; Iwamatsu, A.; Masuda, T.; Shioi, Y.; Takamiya, K. Proc. Natl. Acad. Sci. U.S.A. 94, 333-337, 1997 (7.5pec) (7.
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A;Molecule type: mRNA
A;Residues: 1-525 <8HI>
A;Cross-references: EMBL:U62622; NID:g1805253; PIDN:AAC49624.1; PID:g1805254
A;Experimental source: cv. Aonagajibai; 5 day old seedlings
C;Genetics:
    --- QYFPKTYSGIYRLLACGEFQHDKRYF-MYECVFTQQMRHILQEKQPDIAFCTHALPS 115
                                                                                                 115 IVV----PEYRRRTGRVIPTENVMIDECLHKIWVHENVDKYYVAIDYVKEKLLEIGTHPS 170
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      62 FSIGKQFYRLFYYGVDKIYNKRKFNIYFKMGNKRLGELVDEHQPDIIINTFPM----IV 116
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             314 GLPVRPSFVK--PIRPKIELRKELGMDENLPAVLLMGGGEGMGPIEATAKALSKALYDEN 371
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     5 KRVLILTANYGNGH----VQVAKTLYEQCVRLGFQHVTVSNLYQESNPIVSEVTQYLXLKS 61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  116 YLLNRLKPEYPNLT ----VVNVYTDFFVNOLWGRKNIDYHFVPSTEVKKOLISEGIDQN
                                                                                                                                                                                                                                                                                      171 NVKITGIPIRPQFE----ESMPVGPIYKKYNLSPNKKVLLIMAGAHGV---LKNVKELCE
                                                                                                                                                                                                                                                                                                                                                 G----GXILYKILCGRNEKLYSYVKSLHHPLIEAIPYLHSKAEMNRLYEQATGIMTKPGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           284 ITLTEATAIGVPVILYKPVPGQEKENANFFEDRGAAIVVNRH----EEILESVTSLLADE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                      224 'NLVKDDQVQVVVVCGKNTALKESLSALEAENGDKLKVLGYVERIDELFRITDCMITKPGG
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C; Function:
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Cipecies: Bacer, S.; Bruschi, C.V.; Caldwell, B.; Capuano, V.; Carter, N.M.; Chanture 30, 249-256, 1997
A.; Ehrlich, S.D.; Emmerson, P.T.; Entian, K.D.; Errington, J.; Fabret, C.; Ferrari, E.
Nature 390, 249-256, 1997
A.; Anthors: Poulger, D.; Fritz, C.; Fujita, M.; Fujita, Y.; Fuma, S.; Galizzi, A.; Galler
Lech, J.; Harwood, C.R.; Henaut, A.; Hilbert, H.; Holsappel, S.; Hosono, S.; Hullo, M.F.
Koetter, P.; Koningstein, G.; Krogh, S.; Kumano, M.; Kuita, K.; Lapidus, A.; Laridinois,
A.Authors: Poulger, J.; Lazarevic, V.; Lee, S.M.; Levine, A.; Liu, H.; Masuda, S.; Maueel
Y, M.; Ogawa, K.; Ogivara, A.; Oudega, B.; Park, S.H.; Parro, V.; Pobl, T.M.; Portetelle
Rieger, M.; Rivolta, C.; Rocha, E.; Roche, B.; Rose, M.; Saddie, Y.; Sato, T.; Setonon,
A.Authors: Schletch, S.; Schroeter, R.; Scoffone, F.; Setiguchi, J.; Sekowska, A.; Senor
A.Authors: Poshikawa, H.F.; Zumstein, E.; Yoshikawa, H.; Danchin, A.
A.Title: The complete genome sequence of the Gram-positive bacterium Bacillus subtilis.
A.Accession: B69860
A.Status: preliminary; nucleic acid sequence not shown; translation not shown
A.Residues: 1-373 <a href="https://doi.org/10.1016/j.nuclei.com.nucleic.">doi.org/10.1016/j.nucleic.nucleic.nucleic.nucleic.nucleic.nucleic.nucleic.nucleic.nucleic.nucleic.nucleic.nucleic.nucleic.nucleic.nucleic.nucleic.nucleic.nucleic.nucleic.nucleic.nucleic.nucleic.nucleic.nucleic.nucleic.nucleic.nucleic.nucleic.nucleic.nucleic.nucleic.nucleic.nucleic.nucleic.nucleic.nucleic.nucleic.nucleic.nucleic.nucleic.nucleic.nucleic.nucleic.nucleic.nucleic.nucleic.nucleic.nucleic.nucleic.nucleic.nucleic.nucleic.nucleic.nucleic.nucleic.nucleic.nucleic.nucleic.nucleic.nucleic.nucleic.nucleic.nucleic.nucleic.nucleic.nucleic.nucleic.nucleic.nucl
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       131 VK-HVG--LWSVAFHGTSPKWIHKSYLSALAAYYAKEIEAGLMEYKPDIIISVHPLMQHI 187
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            173 KITGIPIRPQFEES-MPVGPIYKKYNLSPNKKVLLIMAGAHG---VLKNVKELCENLVKD 228
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           60 KSFSIGKQFYRLFYYGVD-KIYNKRKFNIYFKMGNKRLGELVDEHQPDIIINTFPM---- 114
         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  64 IGKQFYRLFYYGVDKI-----YNKRKFNIYFKMGNKRLGELVDEHQPDIIINT--FPM 114
                                                                                        5 KRVLILTANYGNGHVQVAKTLYEQCVRLGF --- QHVTVSNLYQESN -- PIVSEVTQYLYL 59
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              5 KRVLILT-ANYGNGHVQVAKTLYEQCVALGFQHVTVSNLYQESNPIVSEVTQYLYLKSFS 63
                                                                                                                                                                                                                                                                                                                                                                                                                                                            115 -IVVPEYRRRIGRVIPTFNVMTDF-CLHKIWVHENVDKYYVATDYVKEKLLEIGTHPSNV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       : | |::|:||:| | 307 KESNPIGQLIVICGRNKVLASTLASHEWK--IPVKVRGFETQMEKWMGACDCIITKAGPG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TLTEATAIGVPVILYKPVPGQEKENANFFEDRGAAIVVNRHEEILESVTSLLA-DEDTLH
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         32;
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    171; Indels
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    Mismatches
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90;
Conservative
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Best Local Si
Matches 99;
Matches
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Length 468;

14.9%; Score 293; DB 2; 25.1%; Pred. No. 1.3e-12; ive 86; Mismatches 172

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submitted to the EMBL Data Library, July 1998
A; Description: CDNA cloning of an Arabidopsis monogalactosyldiacylglycerol synthase A; Reference number: Z26011
A; Accession: T32269
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     359 GPGTIAESLIRSLPIILNDYIPGQEKGNVPYVVENGAGVFTRSPKETARIVGEWFSTKTD 418
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ----IVVPEYRRRTGRVIPTFNVMTDF-CLHKIWVHENVDKYYVATDYVKEKLLEIGTHP 169
                                                                                                                                                                                                                                                                                                                                                                                                                                  KH---VQLWKVAFHSTSPKWIHSCYLAAIAAYYAKEVEAGL----MEYKPEIIISVHPLM 181
                                                                                                                                                                                                                                                                                                                                                                                                  5 KRVLILTANYGNGHVQVAKTLYEQC-VRLGFQH-VTVSNLYQESN--PIVSEVTQYLYLK 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   241 SQVRVFGLPVRPSFARAVLVKDDLRKELEMDQDLRAVLLMGGGEGMGPVKETAKALEEFL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GGITLTEATAIGVPVILYKPVPGQEKENANFFEDRGAAIVVNRHEEILESVTSLLADE-D
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SFSIGKQFYRLFYYG-----VDKIYNKRKFNIYFKMGNKRLGELVDEHQPDIIINTFPM-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SNVKITGIPIRPQFEESMPV-GPIYKKYNLSPNKKVLLIMAGAHGV--LKNVKELCENLV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       227 KDDQ-----VQVVVVCGKNTALKESLSALEAENGDKLKVLGYVERIDELFRITDCMITKP
                                                                                                              A Molecule type: mRNA
A Residues: 1-468 CAMA>
A CTOSS - references: EMBL:AJ000331; PIDN:CAA04005.1
A Experimental source: cultivar Columbia
C, Genetics:
A Gene: mgd
C; Keywords: glycosyltransferase; hexosyltransferase
                                                                       A;Accession: T52269
A;Status: preliminary; translated from GB/EMBL/DDBJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               341 TLHRMKKNIKDLHLANSSEVILEDILKESE 370
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        | : | : | : | | 419 ELEQTSDNARKLAQPEAVFDIVKDIDELSE 448
                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity 25.19
Matches 98; Conservative
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                                                                                                                                                                                                                                                                      probable 1,2-diacylglycerol 3-beta-galactosyltransferase (EC 2.4.1.46) - Arabidopsis tha N.Alternate names: protein F28M20.30
C.Species: Arabidopsis thaliana (mouse-ear cress)
C.Date: 23-Apr.1999 #sequence_revision 23-Apr-1999 #text_change 11-Jun-1999
                                                                                                                                                                                                                                                                                                                                                                C; Accession: T05092 M; Mueller-Auer, S.; Zipp, M.; Schaefer, M.; Hoheisel, J.; Mewes, R; Bevan, M.; Rieger, M.; Mueller-Auer, S.; Zipp, M.; Schaefer, M.; Hoheisel, J.; Mewes, submitted to the Protein Sequence Database, November 1998 A; Reference number: 215398
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            17;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        I -- VVPEYRRRIG -- RVIPTFNVMTDF-CLHKIWVHENVDKYYVATDYVKEKLLEIGTHP 169
                                                         142 KKVLILMSDTGGGHRASA----EAIRAAFNQEFGDEYQVFITDLWTDHTPWPFNQLPRS 196
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        YLYLKSFSIGKQFYRLFYYGVD-KIYNKRKFNIYFKMGNKRLGELVDEHQPDIIINTFPM 114
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                                286 LTEATAIGVPVILYKPVPGQEKENANFFEDRGAAIVVNRHEEILESVTSLLADE-DTLHR 344
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        254 MQHVPLRVLRSKGLLKKIVFTTVITDLSTCHPTWFHKLVTRCYCPSTEVAKRAQKAGLET
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              5 KRVLILTANYGNGHVQVAKTLYEQCVRLGFQ------HVTVSNLYQESN--PIVSEVTQ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A; Map position: 4
A; ntrons: 175/3; 233/2; 287/2; 334/3; 409/3; 430/3; 455/3
A; Note: F28M20: 30
C; Keywords: glycosyltransferase; hexosyltransferase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match 15.3%; Score 301.5; DB 2; Best Local Similarity 24.8%; Pred. No. 4.1e-13; Matches 101; Conservative 86; Mismatches 172;
                                                                                                                                                                 490 MSQNA--LRLARPDAVFKIVHDLHELVKQ 516
                                                                                                                       MKKNIKDLHLANSSEVI----LEDILKE 368
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A; Molecule type: DNA
A; Residues: 1-533 <BEV>
A; Cross-references: EMBL:AL031004
                                                                                                                                                                                                                                                                                                                                                                                                                                                         Accession: T05092
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A; Status: preliminary
A; Molecule type: DNA
A; Molecule type: DNA
A; Molecule type: DNA
A; Cross-references: EMBL:X64259; NID:g39994; PIDN:CAA45558.1; PID:g39995
B; Miyao, A.; Yoshimura, A.; Sato, T.; Yamamoto, T.; Theeraqool, G.; Kobayashi, Y.
Gene 118, 147-148, 1992
A; Title: Sequence of the Bacillus subtilis homolog of the Escherichia coli cell-divis
A; Reference number: JG1275
A; MulD:92380484
A; Recession: JG1275
A; Molecule type: DNA
A; Residues: 1-180, G', 182-269, T', 271-363 AMIX>
A; Residues: 1-180, G', 182-269, T', 271-363
A; Ressidues: Lukhenhaus, J.
Beall, B.; Lukhenhaus, J.
J. Bacteriol. 171, 6821-6834, 1989
phospho-N-acetylmuramoyl-pentapeptide-transferase (EC 2.7.8.13) - Bacillus subtilis NAlternate names: murG protein; UPD-N-acetylglucosamine--N-acetylmuramyl-(pentapepti C;Species: Bacillus subtilis C;Species: Bacillus subtilis C;Daces: Sacillus subtilis C;Daces: 30-Sep-1993 #sequence_revision 06-Feb-1995 #text_change 20-Jun-2000 C;Accession: S25763; JG1275; S26499; G69662; S22212 R;Henriques, A.; de Lencastre, H.; Piggot, P. R;Henriques, A.; de Lencastre, H.; Piggot, P. A;Title: A Bacillus subtilis morphogene cluster that includes spovE is homologous to A;Reference number: S25762; MUID:93003529
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1.21.ciacylglycerol 3-beta-galactosyltransferase (EC 2.4.1.46) [imported] - Arabidopsis N;Alternate names: monogalactosyldlacylglycerol synthase C;Species: Arabidopsis thaliana (mouse-ear cress) C;Date: 20-0ct-2000 #sequence\_revision 20-0ct-2000 #text\_change 20-0ct-2000 C;Accession: T\$2269 R;Awai, K.; Shimojima, M.; Masuda, T.; Takamiya, K.I.; Ohta, H.

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Nature 392, 353;358, 1998
A,Title: The complete genome of the hyperthermophilic bacterium Aquifex aeolicus.
A;Reference number: A70300; MUID:98196666
A;Accession: C70401
A;Status: preliminary; nucleic acid sequence not shown; translation not shown
A;Molecule type: DNA
A;Residués: 1-344 <AQF>
A;Cross-references: GB:AE000727; NID:92983623; PIDN:AAC07193.1; PID:92983625; GB:AE00
A;Experimental source: strain VF5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               146 ------FPEGVRV-GLPIRKELKKKLPKKEVKRRFGLEPDKITVLIFGGSQGA 191
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            95 RIGELVDEHQPDIIINTFPMIVVPEYRRTGRVIPTFNVMTDFCLHKIWVHENVDKYYVA 154
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NLYQESNPI-----VSEVTQYLYLKSFSIGKQFYRLFYYGVDKIYNKRKFNIYFKMGNK 94
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 62 NFYOKLKAIWKFLKAOEEINEFL-----KEDYRALIFGG---YASLPLGINTVLRRK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               155 TDYVKEKLLEIGTHPSNVKITGIPIRPQFEESMPVGPIYKKYNLSPNKKVLLIMAGAHGV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                215 LKNVKELCENL--VKDDQVQVVVVCGKNTALKESLSALEAENGDKLKVLGYVERIDELFR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              273 ITDCMITKPGGITLTEATAIGVPVILYKPVP----GQEKENANFFEDRGAAIVVNRHEEI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       57; Mismatches 133;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          329 LESVTSLLAD-EDTLHRMKKNIKDLHLANSSEVILEDIL 366
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 195; DB 2;
Pred. No. 4.3e-06;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 9.9%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity 23.38,
Matches, 79; Conservative
     C;Accession: C70401
R;Deckert, G.; Warren, P.V.;
                                                                                                                                                                                                                                                                                                                                                                     A, Gene: murG
C, Superfamily: murG protein
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C;Superfamily: murG protein
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                                                                                               A'Stadues: 16-363 CBEA>
A'Residues: 216-363 CBEA>
A'Rust, F.; Ogasawara, N.; Moszer, I.; Albertini, A.M.; Alloni, G.; Azevedo, V.; Berter C.; Bron, S.; Broullet, S.; Bruschi, C.V.; Caldwell, B.; Capuano, V.; Carter, N.M.; Chd A.; Ehrlich, S.D.; Emmerson, P.T.; Entlan, K.D.; Errington, J.; Fabret, C.; Ferrari, E. Nature 390, 249-256, 1997
A'Authors: Foulger, D.; Fritz, C.; Fujita, M.; Fujita, Y.; Fuma, S.; Galizzi, A.; Galler iech, J.; Haraned, A.; Hilbert, H.; Holsappel, S.; Hosono, M.F. Koetter, D.; Koningstein, G.; Krogh, S.; Kumano, M.; Kurita, K.; Liu, H.; Masuda, S.; Mulco, M.F. Koetter, P.; Koningstein, G.; Krogh, S.; Kumano, M.; Kurita, K.; Liu, H.; Masuda, S.; Mulco, M.F. Koetter, M.; Rivolta, C.; Rocha, E.; Roche, B.; Rosse, M.; Sadaie, Y.; Sacho, T.; Scanlon, A; Authors: Schleich, S.; Schroeter, R.; Scoffone, F.; Sekiguchi, J.; Sekowska, A.; Sero, T.; Alnters, P.; Winters, P.; Winpat, A.; Yamamoto, H.; Yamano, K.; Yasumoto, K.; Yata, K.; Yoshida, K.; Yasumoto, H.; Vasunoto, K.; Yasumoto, K.; Yata, K.; Yata, K.; Yoshida, K.; Ramane, K.; Yasumoto, H.; Danchin, A. A; Reference number: A69580; MUID:98044033
A; Reference number: A69580; MUID:98044033
A; Status, nucleic acid sequence not shown; translation not shown
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A,Residues: 1-363 <KUN>
A,Cross-references: GB:Z99111; GB:AL009126; NID:g2633699; PIDN:CAB13395.1; PID:g2633893
A,Experimental source: strain 168
A;Title: Nucleotide sequence and insertional inactivation of a Bacillus subtilis gene A;Reference number: S26499; MUID:90078133
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              C;Superfamily: murG protein
C;Keywords: glycosyltransferase; hexosyltransferase; peptidoglycan biosynthesis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           20;
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C;Species: Aquifex aeolicus
C;Date: 08-May-1998 #sequence_revision 08-May-1998 #text_change 05-Nov-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          52 EVTOYLYLKSFSIGKOFYRLFYYGVDKI NKRKFNIYFKMGNKRLGELVDEHQPDIIINT 111
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           112 FPMIVVPEYRRRGRVIPTFNVMTDFCLHKIWVHEN-----VDKYYVATDYVKEKLL-- 163
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            -EIGTH-PS-NVKITGIPIRPQFEESMPVGPIYKKYNLSPNKKVLLIMAGAHG---VLKN 217
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                146 EEAKSHFPSEKVVFTGNP-RASEVVSIKTGRSLAEFKLSEDKKTVLIFGGSRGAAPINRA 204
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          VKELCENLVKDDQVQVVVVCGKNTALKESLSALEAEN-GDKLKVLGYVERIDELFRITDC 276
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               58 EITGFKRKLSFENVKTVMR-----FLKGVKKSKSYLAEFKPDAVIGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                100 GGYVCGPVVYAAAKMGIPTI------VHEQNSLPGITNKF--LSKYVNKVAICF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MITKPGGITLTEATAIGVPVILYKPVP----GQEKENANFFEDRGAAIVVNR----HEEI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              80;
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9.9%; Score 196; DB 2; Length 36.
Best Local Similarity 23.1%; Pred. No. 3.9e-06;
Matches 93; Conservative 76; Mismatches 153; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              6 RVLILTANYGNGHVQVAKTLYEQCVRLGFQHVTVSNLY-----
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                                               A; Accession: S26499
A; Status: preliminary
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A;Cross-references: GB:AP001515; GB:BA000004; NID:g10174886; PIDN:BAB06284.1; GSPDB:G
A;Experimental source: strain C-125
                                                                                        Cyaccession: E83970
R;Takami, H.; Nakasone, K.; Takaki, Y.; Maeno, G.; Sasaki, R.; Masui, N.; Fuji, F.;
Nucleic Acids Res. 28, 4317, 4331, 2000
A;Title: Complete genome sequence of the alkaliphilic bacterium Bacillus halodurans A;Reference number: A83650; MUID:20263314
A;Accession: E83970
A;Status: preliminary
A;Molecule type: DNA
UDP-N-acety1glucosamine-N-acety1muramyl- (pentapeptide)pyrophos murg [imported]
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             14;
                                C;Species: Bacillus halodurans
C;Date: 01-Dec_2000 #sequence_revision 01-Dec-2000 #text_change 08-Dec-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         87 IYFKMGNKRLGELVDEHQPDIIINTFPMIVVPEYRRTGRVIPTFNVMTDFCLHKIWVHE 146
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             54; Gaps
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Best Local Similarity 23.1%; Pred. No. 6.7e-05;
Matches 72; Conservative 62; Mismatches 124;
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GB:AE000783; NID:g2688699; PIDN:AAC67113.1; PID:g268
                                                                                                                                                                                                                                                                                              Upp-Nacetylglucosamine--N-acetylmuramyl-(pentapeptide) pyrophosphoryl-undecaprenol 1 C; Species: Borrelia burgdorferi (Lyme disease spirochete)
C; Species: Borrelia burgdorferi (Lyme disease spirochete)
C; Saccession: F70195
R; Fraser, C.M.; Casjens, S.; Huang, W.M.; Sutton, G.G.; Clayton, R.; Lathigra, R.; Wi son, D.; Peterson, J.; Kerlavage, A.R.; Quackenbush, J.; Salzberg, S.; Hanson, M.; Wi Son, D.; Peterson, J.; Kerlavage, A.R.; Quackenbush, J.; Salzberg, S.; Hanson, M.; Wi Suture 390, 580-586, 1997
A; Authors: Smith, H.O.; Venter, J.C.
A; Reference number: A70100; MUID: 98065943
A; Accession: F70195
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    lipopolysaccharide biosynthesis-related protein homolog - Lyme disease spirochete C; Species: Borrelia burgdorferi (Lyme disease spirochete)
C; Date: 13-Feb-1998 #sequence_revision 13-Feb-1998 #text_change 17-Mar-2000
C; Accession: E70156
R; Fraser, C.M.; Casjens, S.; Huang, W.M.; Sutton, G.G.; Clayton, R.; Lathigra, R.; son, D.; Peterson, J.; Kerlavage, A.R.; Quackenbush, J.; Salzberg, S.; Hanson, M.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A; Status: preliminary; nucleic acid sequence not shown; translation not shown
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           59 LKSFSIGKQFYRLFYYGVDKIYNKRKFNIYFK--MGNKRLGELVDEHQPDIIINTFPMIV 116
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TPAI------IASSLLKIKSITHEMDLDPGLATKINSKFANNIHISFKESEKYF 157
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                3 TNKRVLILTANYGNGHV----QVAKTLYEQCVRLGFQHVTVSNLYQESNPIVSEVTQYLY
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 117 VPEYRRRGRVIPTFNVMTDFCLHKIWVHE------NVDKYYVATDYVKEKLLE-IG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       THPSNVKITGIPIRPQFEESMPVGPIYKKYNLSPNKKVLLIMAGAHG--VLKNVKELCEN
                                              258 SGALTVCEIAAVGAAAIF---VPFQHKDRQQYLNAKYLSDVGAAKIIEQADLTPEILVNY
                   ---NANFFEDRGAAIVVNRHE---EILESV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      61;
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8.7%; Score 170.5; DB 2;
Best Local Similarity 20.6%; Pred. No. 0.00022;
Matches 82; Conservative 84; Mismatches 171;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DEDTLHRMKKNIKDLHLANSSEVILEDILKESEMMTAK 375
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                                                                                                                                                       | | : | : | : | : | 315 LKNLTRENLL-QMALKAKTMSMPNAAQRVAEVIKQYS 350
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                                                                                                                            333 TSLLADEDTLHRMKKNIKDLHLANSSEVILEDILKES
                      PGGITLTEATAIGVPVILYKPVPGQEKE-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A; Residues: 1-363 <KLE>
A; Cross-references: GB+AE001176; G
A; Experimental source: strain B31
C; Superfamily: murG protein
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A;Pathway: peptidoglycan biosynthesis
C;Superfamily: murG protein
C;Keywords: cell division; cell wall; glycosyltransferase; hexosyltransferase; peptidogl
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    UDP-N-acetylglucosamine--N-acetylmuramyl-(pentapeptide) pyrophosphoryl-undecaprenol N-ad
C;Species: Haemophilus influenzae
C;Date: 18-Aug-1995 #sequence_revision 18-Aug-1995 #text_change 26-Aug-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                C; Species: Heamophilus influenzae
C; Date: 18-Aug-1995 #sequence_revision 18-Aug-1995 #text_change 26-Aug-1999
C; Date: 18-Aug-1995 #sequence_revision 18-Aug-1995 #text_change 26-Aug-1999
C; Date: 18-Aug-1995 #sequence_revision 18-Aug-1995 #text_change 26-Aug-1999
C; Accession: D64185
R; Fleischmann, R.D.; Fine, W.D.; White, O.; Clayton, R.A.; Kirkness, E.F.; Kerlavage, P. Gocayne, J.D.; Scott, J.; Shirley, R.; Liu, L.I.; Glodek, A.; Kelley, J.M.; Weidman, J.D.; Brandon, R.C.; Fine, L.D.; Fritchman, J.L.; Geoghagen, N.S.M.
Science 269, 496-512, 1995
A; Authors: Gnehm, C.L.; McDonald, L.A.; Small, K.V.; Fraser, C.M.; Smith, H.O.; Venter, A; Reference number: A64000; MUID:95350630
A; Reference number: A64000; MUID:95350630
A; Accession: D64185
A; Accession: D64185
A; Accession: D64186
A; Molecule type: DNA
A; Residues: 1-351 CTIGR>
A; Residues: 1-351 CTIGR>
A; Cross_references: GB:U32793; GB:L42023; NID:q1574683; PIDN:AAC22793.1; PID:g1574693;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   117 VPEYRRRIGRVIPTFNVMIDFCLHKIWVHENVDKYYVAIDYVKEKLL-EIGT-----HPS 170
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ---NVKITGIPIRPQFEESMPVGPIYKKYNLSPNKKVLLIMAGA-----HGVLKNVKE 220
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        149 AFPHAEVVGNPVREDLFE-MPNPDI--RFSDREEKLRVLVVGGSQGARVLNHTLPKVVAQ 205
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                                                                                                                                                                                                                                                                                                                                                                                               N-----VDKY---YVATDYVKEKLLEIGTHPSNVKITGIPIRPQF----EESMPVGPI 192
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                                                                                                                                                                                                                                                                                            -GQEKENANFFEDRGAAIVVNRHE----EILESVTSLLADEDTLHRMKKNIKDLHLANSS
                                                                                                                                                          193 YKKYNLSPNKKVLLIMAGAHGVLKNVKELCENLVKDDQV---QVVVVCG--KNTALKESL
                                                                                                   123 ONSVPGLTNKFLSRYVDRIAICFKEAEAFFPKNKVVFTGNPRASEVMSGNREEGL----
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75 VRFLRGTKRAKALLNEFKPDVVIGTGGYVCGPVVYAAAKLKIPTV-
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EKLHMLVKEVAK 363
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Best Local S.
Matches 95
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L--VKDDQVQVVVVCGK--NTALKESLSALEAENGDKLKVLGYVERIDELFRITDCMITK 280
                                                                                                                                                                                                          281 PGGITLTEATAIGVPVILYKPVPG----OEKENANFFEDRGAAIVVNRHEEILESVTSLL 336
                                                          ----PSNVKITGIPIRPQFEESMPVGPIYKKYNLSPNKKVLLIMAGAHGVLKNVKELCEN
                                                                                                                                                                     LPELAGRSFKTVYASGEIYYDDYKETFN--QYKENSNLDIRPYINNMTELLAKSQLFLGR
                                                                                           150 QYFPASKTTFTG---NPRAQEVADAAAQVEKF----EEPTVVIFGGSRGALKLNNAFIEA
                                                                                                                                                                                                                               SGSTTTAEVTALGLPAV-YVPSPNVTADQOTKNAOEYVDOGAAIIIK---
                                                                                                                                                                                                                                                                                                                   -DED------LTGQTLVEAISNILENNEKYQEMQAASLKAGV 341
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C;Species: Lactococcus lactis subsp. lactis
C;Date: 23-Mar-2001 #sequence_revision 23-Mar-2001 #text_change 31-Mar-2001
C;Accession: E86823
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 R;Bolotin, A.; Wincker, P.; Mauger, S.; Jaillon, O.; Malarme, K.; Weissenbach, J.; Ehrl;
Genome Res. in press, 2001
A;Tille: The complete genome sequence of the lactic acid bacterium.
A;Reference number: A86625
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S.; Fujii, C.; Cotton, M.D.; Horst, K.; Roberts, K.; Hatch,
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A:Cross-references: GB:AE005176; NID:g12724594; PIDN:AAK05687.1; GSPDB:GN00146
A:Experimental source: strain IL1403
         223 THL-KDLLMQNNNYKLILIGKGSEEKE-IKNFSIKHGLEKQILLIGTIPWEEIYYYYKIS 280
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     281 DIFASLSKSEVYPMTVIEALTAGIPAILINDYIYKDV---IKEGINGF-----LIKKY 330
                                                                                                                                                                                                                                                                                                                                74 YGVDKIYNKRKFNIYFKMGNKR-LGELVDEHQPDII--INTFPMIVVPEYRRTGR---- 126
                                                                                                                                                                                                                                                                                                                                                          ---HENVDKYYV-ATDYVKEKLLEIGT 167
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TQYLYLKSFSIGKQFYRLFYYGVDKIYNKRKFNIYFKMGNKRLGELVDEHQPDIIINTFP 113
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Pred. No. 0.0013;
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Matches 80; Conservative
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Matches 72; Conserva
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Status: preliminary
Molecule type: DNA
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GenCore version 4.5
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OM protein - protein search, using sw model

June 29, 2001, 08:59:08; Search time 16.33 Seconds (without alignments) 801.322 Million cell updates/sec Run on:

US-09-668-788-2 1970 1 MNFNKRVLILTANYGNGHVQ......EDILKESEMMTAKQKAKVLS 382 Title: Perfect score: Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5

Scoring table:

Searched:

93435 Total number of hits satisfying chosen parameters:

93435 segs, 34255486 residues

Minimum DB seq length: 0 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

SwissProt\_39:\* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

		P54166 bacillus su		O67238 aquifex aeo	_	P45065 haemophilus		007670 enterococcu	Q9x4h4 streptomyce	Q9zba5 streptomyce	069552 mycobacteri		_	Q9zk59 helicobacte	-	₹*	3 escherich				Q41607 tulipa gesn		P74657 synechocyst	P31927 zea mays (m	_	5	~	P42982 bacillus su	Q62452 mus musculu	P77886 lactobacill	P39928 saccharomyc	3802	8454	Q58295 methanococc
SUMMARIES	ID	YPFP_BACSU	MURG_BACSU	MURG_AQUAE	MURG_ENTFA	MURG_HAEIN	MURG_BORBU	MURG_ENTHR	MURG_STRCU	MURG_STRCO	MURG_MYCLE	MURG_HELPY	YA62_METJA	MURG_HELPJ	MURG_MYCTU	NIFE_ANASP .	MURG_ECOLI	MURG_THEMA	MURG_RICPR	YVYH_BACSU	SUS2_TULGE	MURG_BUCAI	MURG_SYNY3	SPS_MAIZE	UD16_RAT	RBP2_PLAVB	RFAB_ECOLI	YPJH_BACSU	UD17_MOUSE	CARB_LACPL	SLN1_YEAST	SPS_ORYSA	YC08_KLEPN	DPOL_METJA
	DB	1	Т	Н	7	٦	-	٦	7	٦	7	٦	-	-	-	-	Н		-	-		<b>~</b>	<b>-</b>	Н	Н	Н	-	-	Н	-	~	Н		~
	Length	382	363	344	363	351						353	484	353	410	480	354	339	382	380	820	354	371	1068	529	1251	369	377	520	1058	1220	1049	373	1634
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	Score		196	195	185.5	171	170.5	161.5	138.5	137.5	137.5	136	135	134	128.5	123.5	123	122.5	121.5	117.5	116	113.5	113	112.5	110	106	105.5	105.5	105.5	105.5	105.5	105	104	104
	Result No.	1	7	٣	4	S	9	7	80	σ	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	26	27	28	29	30	31	32	33

Q40287 manihot esc O64435 mus musculu	P49034 alnus gluti Q25225 leishmania	Q58884 methanococc	P27828 escherichia	P70691 mus musculu P49031 beta vulgar	004932 craterostig Q02455 saccharomyc	
UFO5_MANES UD16_MOUSE	SUSY_ALNGL IF4A_LEIBR	VESS_METJA	WECB_ECOLI	UD12_MOUSE SPS_BETVU	SPS1_CRAPL MLP1_YEAST	
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34 35	37	9 6 6	444	4 4 3 8	4 4 5	

# ALIGNMENTS

	ALIGNMENTS
RESU YPFP ID	RESULT 1 YPFP_BACSU ID YPFP_BACSU STANDARD; PRT; 382 AA.
S F F	P54166; 01-607-1996 (Rel. 34, Created) 01-607-1996 (Rel. 34, Last sequence undate)
담	(Rel. 39, 43.6 KDA
N S	
888	Bactiles Firmicutes, Bacillus/Clostridium group;
0 X	Bacitlus/Staphylococcus group; Bacillus. NCBD TaxID=1423:
Z.	
RP X	SEQUENCE FROM N.A. MEDITURE 96349105. DubWed#8760912.
RA	Sorokin A.V., Azevedo V., Zumstein E., Galleron N., Ehrlich S.D.,
RA F	Serror P.; "Somiono and unit of the Bandillin miktille absonment worden between
RT	Sequence analysis of the bacillus subtilis chromosome region between the serA and kdg loci cloned in a yeast artificial chromosome.";
RL	Microbiology 142:2005-2016(1996).
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35	This CWICG-DROW ontry is convright. It is produced through a collaboration
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36	use by non-proint institutions as long as its content is in no way modified and this statement is not removed. Heare hy and for commercial
ខ	entities requires a license agreement (See http://www.isb-sib.ch/announce/
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Z E	EMBL; 1/1/46; AAA9624.1;
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ă ă	Tuterpro: TPR001296: -
DR	Pfam; PF00534; Glycos_transf_1; 1.
KW SQ	Hypothetical protein, Transferase, Glycosyltransferase. SEQUENCE 382 AA, 43561 MW; 8A8B98593DAC6041 CRC64;
D O M	Query Match 100.0%; Score 1970; DB 1; Length 382; Best Local Similarity 100.0%; Pred. No. 9.8e-129; Matches 382: Conservative 0: Mismatches 0: Indels 0: Gans 0:
•	
ολ	-
q	1 MNTNKRVLILITANYGNGHVQVAKTLYEQCVRLGFQHVTVSNLYQESNPIVSEVTQYLYLK 60
οy	61 SFSIGKQFYRLFYYGVDKIYNKRKFNIYFKMGNKRLGELVDEHQPDIIINTFPMIVVPEY 120
q	61 SFSIGKÇFYRLFYYGVDKIYNKRKFNIYFKMGNKRLGELVDEHQPDIIINTFPMIVVPEY 120
Οy	121 RRRIGRVIPTFNVMIDFCLHKIWVHENVDKYYVATDYVKEKLLEIGTHPSNVKITGIPIR 180
qa	121 RRRIGRÝIPTENVMIDECLHKIWVHENVDKYXVATDYVKEKLLEIGTHPSNVKITGIPIR 180

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RESULT 3
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"Nucleotide sequence and insertional inactivation of a Bacillus subtilis gene that affects cell division, sporulation, and temperature sensitivity.";

J. Bacteriol. 171:6821-6834(1989).

-!-FORVION: CELL WILL FORMATION. CATALYZES THE TRANSFER OF A GLCNAC SUBUNIT ON UNDECAPRANYL-PROPHOSPHORYL-MURNAC-PENTAREPTIDE (LIPID INTERMEDIATE I) TO FORM UNDECAPRENYL-PROPHOSPHORYL-MURNAC-PENTAREPTIDE (LEPID INTERMEDIATE II).

-!- PATHWAY: LAST STEP OF PEPTIDOGLYCAN BIOSYNTHESIS.

-!- SUBCELLULAR LOCATION: MEMBRANE ASSOCIATED (BY SIMILARITY).
                                                                      241 TALKESLSALEAENGDKLKVLGYVERIDELFRITDCMITKPGGITLTEATAIGVPVILXK 300
                                                                                                                                                                                                                                                                   P37585; P18578; O59247;
01-NOV-1990 (Rel. 16, Created)
30-MAY-2000 (Rel. 39, Last sequence update)
30-MAY-2000 (Rel. 39, Last annotation update)
30-MAY-2000 (Rel. 39, Last annotation update)
PUDP-N-ACETYLAGUCOSAMIRE--N-ACETYLAGUCOSAMIRE TRANSFERASE
(EC 2.4.1.-) (UNDECAPRENTL-PP-MURNAC-PENTAPEPTIDE-UDPGICNAC GLCNAC TRANSFERASE).
              241 TALKESLSALEAENGDKLKVLGYVERIDELFRITDCMITKPGGITLTEATAIGVPVILYK
                                                                                                               PVPGQEKENANFFEDRGAAIVVNRHEEILESVTSLLADEDTLHRMKKNIKDLHLANSSEV
PQFEESMPVGPIYKKYNLSPNKKVLLIMAGAHGVLKNVKELCENLVKDDQVQVVVVCGKN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     subtilis homolog of the Escherichia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
MEDLINE-92380484; PubMed-1387377;
Miyao A., Yoshimura A., Sato T., Yamamoto T., Theeragool G.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Henriques A.O., de Lencastre H., Piggot P.J:;
A Bacillus subtills morphogene cluster that includes spoVE
homologous to the mra region of Escherichia coli.";
Biochimie 74:735-748(1992).
                                                                                                                                                                                                                                                                                                                                                                                                                          Bacteria; Firmicutes; Bacillus/Clostridium group; Bacillus/Staphylococcus group; Bacillus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SIMILARITY: BELONGS TO THE MURG FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDLINE=93003529; PubMed=1391053;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE OF 216-363 FROM N.A. MEDLINE-90078133; PubMed-2556375;
                                                                                                                                                                                     361 ILEDILKESEMMTAKQKAKVLS 382
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     "Sequence of the Bacillus s
cell-division gene murG.";
Gene 118:147-148(1992).
                                                                                                                                                                                                                                                                                                                                                                                                             Bacillus subtilis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                        NCBI_TaxID=1423;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Kobayashi Y
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STRAIN=168
                                                                                                                                           301
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Nature 392:353-358(1998).
-i- FUNCTION: CELL WALL FORMATION. CATALYZES THE TRANSFER OF A GLCNAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             277 MITKPGGITLTEATAIGVPVILYKPVP----GQEKENANFFEDRGAAIVVNR----HEEI 328
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EVTQYLYLKSFSIGKQFYRLFYYGVDKIYNKRKFNIYFKMGNKRLGELVDEHQPDIIINT 111
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             112 FPMIVVPEYRRRIGRVIPTFNVMTDFCLHKIWVHEN-----VDKYYVATDYVKEKLL-- 163
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30-MAY-2000 (Rel. 39, Last sequence update)
30-MAY-2000 (Rel. 39, Last annotation update)
UDP-N-ACETYLGLUCOSAMINE--N-ACETYLUNGAMIL-(PENTAPEPTIDE)
PYROPHOSPHORYL-UNDECAPRENOL N-ACETYLUCOCOSAMINE TRANSFERASE
(EC 2.4.1.-) (UNDECAPRENYL-PP-MURNAC-PENTAPEPTIDE-UDPGLCNAC GLCNAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  -EIGTH-PS-NVKITGIPIRPQFEESMPVGPIYKKYNLSPNKKVLLIMAGAHG---VLKN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 218 VKELCENLVKDDQVQVVVVCGKNTALKESLSALEAEN-GDKLKVLGYVERIDELFRITDC
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Deckert G., Warren P.V., Gaasterland T., Young W.G., Lenox A.L.,
Deckert G., Warren P.V., Gaasterland T., Young W.G., Lenox A.L.,
Forham D.E., Overbeek R., Snedd M.A., Keller M., Aujay M., Huber
Feldman R.A., Short J.M., Olson G.J., Swanson R.V.;
"The complete genome of the hyperthermophilic bacterium Aquifex
                                                                                                                                                                                                                                                                                                                                                                                                                                                         80;
                                                                                                                                                                                                                                                                                                                                                                                                Length 363;
                                                                                                                                             PIR; S26499; S26499.
SubtiList; BG10227; murG.
Transferase; Glycosyltransferase; Cell division; Cell wall;
                                                                                                                                                                                                                                                                                                                                                                                                                                                            Indels
                                                                                                                                                                                                                                                      81 K -> G (IN REF. 1).
270 A -> T (IN REF. 1).
39977 MW; 185B2068BC732489 CRC64;
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IEALDRIVLNEOTLKEMSERTKSLGVPDAAARLYSVLEELKK 363
                                                                                                                                                                                                                                                                                                                                                                                                   9.9%; Score 196; DB 1; 23.1%; Pred. No. 1.4e-06; iive 76; Mismatches 153.
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                                                                                                                                                                                                                                    Membrane; Peptidoglycan synthesis.
EMBL; D10602; BAA01454.1; -.
EMBL; X64229; CAA45558.1; -.
EMBL; M31827; AAA83968.1; -.
EMBL; Z99111; CAB13395.1; -.
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                                                                                                                  JC1275; JC1275.
S26499; S26499.
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270 2
363 AA;
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Aquifex aeolicus
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CONFLICT
SEQUENCE
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MURG OR HI1138
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J. Bacteriol.
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Best Local Simi
Matches 91;
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P45065;
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MURG_HAEIN
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                                                                                               This SWISS-PROT entry is copyright. It is produced through a collaboration between the SAISS Institute of Bioinformatics and the EMED outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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UNDECAPRENYL-PYROPHOSPHORYL-MURNAC-PENTAPEPTIDE (LIPID
                                                                                                                                                                                                                                                                                                                                                                                                  62 NFYOKLKAIWKFLKAQEEINEFL-----KEDYRALIFGG---YASLPLGINTVLRRK 110
                                                                                                                                                                                                                                                                                                                                                                                                                               95 RLGELVDEHQPDIIINTFPMIVVPEYRRTGRVIPTFNVMTDFCLHKIWVHENVDKYYVA 154
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           214
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                                                                                                                                                                                                                                                                                                                                                                       41 NLYQESNPI-----VSEVTQYLYLKSFSIGKQFYRLFYYGVDKIYNKRKFNIYFKMGNK 94
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    30-MAY-2000 (Rel. 39, Created)
30-MAY-2000 (Rel. 39, Last sequence update)
30-MAY-2000 (Rel. 39, Last annotation update)
UDP-N-ACETYLGLUCOSAMINE-N-ACETYLMURANYL-(PENTAPEPTIDE)
PYROPHOSPHORYL-UNDECAPRENDL N-ACETYLGLUCOSAMINE TRANSFERASE
(EC 2.1.1.) (UNDECAPRENTL-PP-MURNAC-PENTAPEPTIDE-UDPGLCNAC GLCNAC TRANSFERASE)
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Bacteria; Firmicutes; Bacillus/Clostridium group; Enterococcaceae;
          INTERMEDIATE I) TO FORM UNDECAPRENTI-PYROPHOSPHORYL-MURNAC-
(PENTAPEPTIDE)GLCNAC (LIPID INTERMEDIATE II) (BY SIMILARITY).
PATHWAY: LAST STEP OF PEPTIDOGLYCAN BIOSYNTHESIS.
SUBCELLULAR LOCATION: MEMBRANE ASSOCIATED (BY SIMILARITY).
SIMILARITY: BELONGS TO THE MURG FAMILY.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          273 ITDCMITKPGGITLTEATAIGVPVILYKPVP----GQEKENANFFEDRGAAIVVNRHEEI
                                                                                                                                                                                                                                                                                                                                           70;
                                                                                                                                                                                                                    EMBL; AE000727; AAC07193.1; Transferase; Glycosyltransferase; Glycosyltransferase; Cell division; Cell wall;
                                                                                                                                                                                                                                                                                                             Length 344;
                                                                                                                                                                                                                                                                                                                                                                                                                                                            111 EL--FIHEQ-----NSIPSKINKILSKKAKKVLITFNYTKRF------
                                                                                                                                                                                                                                                                                                                                           Indels
                                                                                                                                                                                                                                                                 5A4B3322B4AC650C CRC64;
                                                                                                                                                                                                                                                                                                          9.9%; Score 195; DB 1; Lv
23.3%; Pred. No. 1.5e-06;
iive 57; Mismatches 133;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     329 LESVTSLLAD-EDTLHRMKKNIKDLHLANSSEVILEDIL 366
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 305 PDKVLSALKEIVKNLERYSENIKKFFAEGAEERMYEELL 343
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           363 AA.
                                                                                                                                                                                                                                                  Membrane; Peptidoglycan synthesis.
SEQUENCE 344 AA; 39325 MW; 5A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDLINE-97431524; PubMed-9287029;
                                                                                                                                                                                                                                                                                                                                         Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STANDARD;
                                                                                                                                                                                                                                                                                                                           Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NCBI_TaxID=1351;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STRAIN-A24836
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Enterococcus
                                                                                                                                                                                                                                                                                                                                        79;
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                                                                                                                                                                                                                                                                                                             Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                   use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           13
sters in pathogenic gram-positive cocci.";

Bacteriol. 179:5612-5635(1997).

FUNCTION: CELL WALL FORMATION. CATALYZES THE TRANSFER OF A GLCNAC SUBUNIT ON UNDECAPRENTL-PYROPHOSPHORYL-MURNAC-PENTAPEPTIDE (LIPID INTERMEDIATE I) TO FORM UNDECAPRENYL-PYROPHOSPHORYL-MURNAC-PENTAPEPTIDE)GLCNAC (LIPID INTERMEDIATE II) (BY SIMILARITY).

PATHWAY: LAST STEP OF PEPTIDOGLYCAN BIOSYNTHESIS.

SUBCELLULAR LOCATION: MEMBRANE ASSOCIATED (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              260 NTDLMVGRAGATSIAEFTALGLPAIL---IPSPYVTNDHQTKNAQSLVKVGAVEMIPDA- 315
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              157
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     217
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              201 INQAFEQAFPLFEEREYÖVLYASGERYYÖELQESLK-LSEKKLTNISVOPYIDKMVEVMA 259
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             62
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   01-NOV-1995 (Rel. 32, Last sequence update)
30-MAY-2000 (Rel. 39, Last annotation update)
UDP-N-ACETYIGLUCOSAMINE-N-ACETYLAURANYL-(PENTAREPTIDE)
PYROPHOSHORYL-UNDECAPRENOL N-ACETYLAUCOSAMINE TRANSFERASE
(EC 2.4.1.-) (UNDECAPRENYL-PP-MURNAC-PENTAREPTIDE-UDPGLCNAC GLCNAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              8 LILTANYGNGHVQVAKTLYE----QCVRLGFQHV-TVSNLYQESNPIVSEVTQYLYLKSF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    63 --SIGKQFYRLFYYGVDKIYNKRKFNIYFKMGNKRLGELVDEHQPDIIINTFPMIVVPEY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 -VDKYY - - - - - VATDY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              104 ---SGAVV----YAAHQLKIPTIIHEQNSIPGMTNKFLSRYVDKIAICFPDVASFF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 VKEKLLEIGTHPSNVKITGIPIRPQFEESMPVGPIYKKYNLSPNKKVLLIMAGAHGVLKN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           218 VKELCEN---LVKDDQVQVVVVCGKN--TALKESLSALEAENGDKLKVLGYVERIDELFR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     273 ITDCMITKPGGITLTEATAIGVPVILYKPVPGQEKENANFFEDRGAAIVVNRHEEILESV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          3 ILVIGGGIGGHIYPALSFVEHVKKEAPATEFLYVGTENGLESQIVPKAKIPFKTIKIQGF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       97;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 363;
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Haemophilus.
NCBI_TaxID=727;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Transferase; Glycosyltransferase; Cell division; Cell wall; Membrane; Peptidoglycan synthesis.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               -----ELTGARLVAAIDDILLNNE------KRQQMATASKGERI 348
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Peptidoglycan synthesis.
363 AA: 39916 MW; 5178BCC95264BE69 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   76; Mismatches 144;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DB 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                9.4%; Score 185.5; DB 1 22.3%; Pred. No. 7.2e-06;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RRRIGRVIPTFNVMTDFCLHKI----WVHEN-----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EMBL; U94707; AAC45636.1; -
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MURG_BORBU
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                  SOUR DESCRIPTION OF COLOR COLO
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its most by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entitles requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@lsb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 22;
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                                                                                                                                                                                                                                                                                                                                                                                                            57 LYLKSFSIGKQFYRLFYYGVDKIYNKRKFNIYFKMGNKRLGELVDEHQPDIIINTFPMIV 116
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              117 VPEYRRTGRVIPTFNVMTDFCLHKIWVHENVDKYYVATDYVKEKLL-EIGT----HPS 170
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               100 -----MGGYVSGPAGVAAKLCGVPIILHEQ-----NAIAGLINKLLGKIATCVLQAFPT 148
                                                                                                                                                                                                                                                                                                                                             influenzae Rd.";
Science 269:496-512(1995).
-i- FUNCTION: CELL WALL FORMATION. CATALYZES THE TRANSFER OF A GLCNAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         3 NKKLLVMAGGTG-GHVFPAIAVAQTLQKQEWDICWLG----TKDRMEAQLVPKYGIPIRF 57
                            STRAIN-RD / KW20 / ATCC 51907;

STRAIN-RD / KW20 / ATCC 51907;

RELEISCHMann R.D., Adams M.D., White O., Clayton R.A., Kirkness E.F., Rerlavage A.R., Bult C.J., Tomb J.F., Dougherty B.A., Merrick J.M., McKenney K., Sutton G., Fitzhugh W., Fields C.A., Gocayne J.D., McKenney K., Shirley R., Liu L.-I., Glodek A., Kelley J.M., Weidman J.F., Phillips C.A., Spriggs T., Hedblom E., Cotton M.D., Utterback T.R., Hanna M.C., Nguyen D.T., Saudek D.M., Brandon R.C., Grehm C.L., Fritchman J.L., Fubraman J.L., Geoghagen N.S. M., Gnehm C.L., McDonald L.A., Small K.V., Fraser C.M., Smith H.O., Venter J.C.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 149 AFPHAEVVGNPVREDLFE-MPNPDI--RFSDREEKLRVLVVGGSQGARVLNHTLPKVVAQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 221 LCENLVKDDQVQVVVVCGKNTALKESLSALEAENGDKLKVLGYVERIDELFRITDCMITK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               281 PGGITLTEATAIGVPVILYKPVPGQEKE----NANFFEDRGAAIVVNRHE---EILESV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               58 IQISGLR-GK-----GIKALLN-APFAIFRAVLOAK--KIIQEEKPDAVLG-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 80;
                                                                                                                                                                                                                                                                                                                   "Whole-genome random sequencing and assembly of Haemophilus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Cell wall;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 351;
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Inner membrane; Membrane; Peptidoglycan synthesis.
SEQUENCE 351 AA; 38307 MW; 41067F379BB30B27 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               8.7%; Score 171; DB 1; I
23.9%; Pred. No. 6.8e-05;
tive 72; Mismatches 150;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          333 TSLLADEDTLHRMKKNIKDLHLANSSEVILEDILKES 369
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EMBL; U32793; AAC22793.1; -.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STRAIN-ATCC 35210 / B31;

STRAIN-ATCC 35210 / B31;

MEDLINE-98065943; PubMed-9403685;

Fraser C.M., Casjens S., Huang W.M., Sutton G.G., Clayton R.A.,

Lathigra R., White O., Ketchum K.A., Dodson R., Hickey E.K., Gwinn M.,

Dougherty B., Tomb J:-F., Fleischmann R.D., Richardson D.,

Peterson J., Kerlavage A.R., Quackenbush J., Salzberg S., Hanson M.,

van Vugt R., Palmer N., Adams M.D., Gocayne J.D., Weidman J.,

Utterback T., Watthey L., McDonald L., Artlach P., Bowman C.,

Garland S., Puji C., Cotton M.D., Horst K., Roberts K., Hatch B.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LVKDDQVQVVVVCGKNTALKESLSALEAENGDKLKVLGYVERIDELFRITDCMITKPGGI 284
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FUNCTION: CELL WALL FORMATION. CATALYZES THE TRANSFER OF A GLCNAC GEDUNIT ON UNDECAPRENTAL-PETIDE (LIPID INTERMEDIATE I) TO FORM UNDECAPRENTYL-PEROPHOSPHORYL-MURNAC-FERNAREPETIDE (LIPID INTERMEDIATE I) (BY SIMILARITY).

(PENTARAPETIDE)GLCNAC (LIPID INTERMEDIATE II) (BY SIMILARITY).

SUBCELLULAR LOCATION: MEMBRANE ASSOCIATED (BY SIMILARITY).

SIMILARITY: BELONGS TO THE MURG FAMILY.
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                                                         30-MAY-2000 (Rel. 39, Created)
30-MAY-2000 (Rel. 39, Last sequence update)
30-MAY-2000 (Rel. 39, Last annotation update)
UDP-N-ACETYLGLUCOSAMINE--N-ACETYLMURAMYL-(PENTAPEPTIDE)
PYROPHOSPHORYL-UNDECAPRENOL N-ACETYLGLUCOSAMINE TRANSFERASE
(EC 2.4.1.-) (UNDECAPRENYL-PP-MURNAC-PENTAPEPTIDE-UDPGLCNAC GLCNAC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      110 TPAI------IASSLLKIKSITHEMDLDPGLATKINSKFANNIHISFKESEKYF
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Smith H.O., Venter J.C.;
"Genomic sequence of a Lyme disease spirochaete, Borrella
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Indels
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SEQUENCE 363 Aa; 41118 MW; 1BAFA347384DB235 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                             Bacteria; Spirochaetales; Spirochaetaceae; Borrelia
                                                                                                                                                                                                                                                                                                                                                                                        Borrelia burgdorferi (Lyme disease spirochete)
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363
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PRT;
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Best Local Similarity 20.6
Matches 82; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Nature 390:580-586(1997).
STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NCBI_TaxID-139;
                                                                                                                                                                                                                                                                                                                                                        MURG OR BB0767
                                                                                                                                                                                                                                                                                                                   PRANSFERASE
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Ouery Match
Best Local Similarity
Matches 46; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STRAIN-DSM 40733;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MURG_STRCU
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                                                                                                                                      KIVPETGMPFRTLEIQGFQRKLSLHNLKTIQLFLK-SIREAKKILKEFKPDVVIGTGGYV 103
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30-MAY-2000 (Rel. 39, Last annotation update)
UDP-N-ACETYLGHOCOSAMINE-N-ACETYLGHOCOSAMINE)
PYROPHOSPHORYL-UNDECAPRENOL N-ACETYLGHOCOSAMINE TRANSFERASE
(EC 2.4.1.) (UNDECAPRENYL-PP-MURNAC-PENTAPEPTIDE-UDPGLCNAC GLCNAC TRANSFERASE).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Bacteria; Firmicutes; Bacillus/Clostridium group; Enterococcacea;
                                                                                                TLTEATAIGVPVILY - - - KPVPGQEKENANFFEDRGAAIVVNRHE - - - - EILESVTSLLA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      8 LILTANYGNGHVQVAKTLYEQCVRLGFQHVTVSNLYQESNPIVSEVTQYLYLKSF----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Mismatches 149; Indels 105;
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SEQUENCE 360 AA; 39591 MW; 444D6F7CFEC1FDA1 CRC64;
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                                                                                                                                                                                                                                                                     | : :: :|:||| : :|| : :|| : :|| : || DREKINSLKENIKKFNNKHSSTLIAKLLIKDIKETKSK 363
                                                                                                                                                                                                                               DEDTLHRMKKNIKDLHLANSSEVILEDILKESEMMTAK 375
                                                                                                                                                                                                                                                                                                                                                                                                                                                               360 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                               STANDARD;
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MURG_ENTHR
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ---YVTNDHQ--TKNAMSLV 299
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        158 HPVRRSIATLDRAAVRPEAR-----ARFGLDPNLPTLLVSGGSQGARRLNEVVQQV 208
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30-MAY-2000 (Rel. 39, Last sequence update)
30-MAY-2000 (Rel. 39, Last annotation update)
UDP-IN-ACETYLGLUCOSAMINE--N-ACETYLMURAMYL-(PENTAPEPTIDE)
PYROPHOSPHOKYL-UNDECAPRENOL N-ACETYLGLUCOSAMINE TRANSFERASE
(BC 12.4.1.*) (UNDECAPRENYL-PP-MURNAC-PENTAPEPTIDE-UDPGLCNAC GLCNAC
                                   Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;
Actinomycetales; Streptomycineae; Streptomycetaceae; Streptomyces.
                                                                                                                  NVKELČENLVKDDQVQVVVVCGKNTALKESLSALEAENGDKLKVLGYVERIDELFRITDC
                                                                                                                                                                            201 INQAVTEFLMSFDQEYQVLYASGERYYKDIQTKVPA--CANVSIQPYINKMAEVMASSDL
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YVKEKLLEIGTHPSNVKITGIPIRPQFEESMPVGPIYKKYNLSPNKKVLLIMAGAHGVLK
                                                                                                                                                                                                                                  277 MITKPGGITLTEATAIGVPVILYKPVPGQEKENANFFEDRGAAIVVNRHEEILESVTSLL
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47; Mismatches
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SEQUENCE 362 AA; 38847 MW; OBI
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SUBCELLUIAR LOCATION: MEMBRANE ASSOCIATED (BY SIMILARITY).
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01-0CT-2000 (Rel. 40, Last annotation update)
01-PA-ACETYLGLUGOSAMINE-N-ACETYLUMRAMYL (PENTAPEPTIDE)
PYROPHOSPHORYL-UNDECAPRENOL N-ACETYLGLUGOSAMINE TRANSFERASE
(EC 2.4.1.-) (UNDECAPRENYL-PP-MURNAC-PENTAPEPTIDE-UDPGLCNAC GLCNAC
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Saunders D.C., Harris D., James K.D., Parkhill J., Barrell B.G.,
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Submitted (JAN-1999) to the EMBL/GenBank/DDBJ databases
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Submitted (AUG-1999) to the EMBL/GenBank/DDBJ databases
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Streptomyces coelicolor.
Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;
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                                                                                                                                                                                                                                                                                                                                   STRCO
                                                                 265
                                                                                                                                                                                                                                                                                                                                      MURG
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for commercial
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FUNCTION: CELL WALL FORMATION CAPALYZES THE TRANSFER OF A GLUNAC SUBUNIT ON UNDECARRANDE CAPALYZES THE TRANSFER OF A GLUNAC INTERMEDIATE I) TO FORM UNDECAPRINYL-PYROPHOSPHORYL-WURNAC-PENTAPEPTIDE (LIPID INTERMEDIATE I) TO FORM UNDECAPRINYL-PYROPHOSPHORYL-WURNAC-PENTAPEPTIDE (LIPID STRUMAY) I LAST STEP OF PEPTIDOGLYCAN BIOSYNTHESIS.

SUBCELLULAR LOCATION: MEMBRANE ASSOCIATED (BY SIMILARITY).

SIMILARITY: BELONGS TO THE MURG FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            216
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            VATDY---VKEKLLEI--GTHPSNVKITGIPI------RPQFEESMPVGPIYKKYNLS 199
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            KLKV-LGYVERIDELFRITDCMITKPGGITLTEATAIGVPVILYKPVP---GQEKENANF 312
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               117 EVVEAH----VVVGFGGYVALPAYLAARGIPRVRRRIP--------VVVHEANARAG 161
GLDPNLPTLLVTGGSQGA-RRLNEVIQQVAPWLQQAGIQILHAVGP----KNELPQVHQM 235
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Actinomycetales; Corynebacterineae; Mycobacteriaceae; Mycobacterium
                                                                                                                                                                                                                                                                                                                                                                                                                                                  30-MAY-2000 (Rel. 39, Created)
30-MAY-2000 (Rel. 39, Last sequence update)
30-MAY-2000 (Rel. 39, Last annotation update)
UDP-N-ACETYLGLUCOSAMINE-N-N-ACETYLMRAMIL-(PENTAPEPTIDE)
PYROPHOSPHORYL-UNDECAPRENOIL N-ACETYLGLUCOSAMINE TRANSFERASE
(EC 2.4.1.-) (UNDECAPRENOIL-PP-MURNAC-PENTAPEPTIDE-UDPGLCNAC GLCNAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PNKKVLLIMAGAHGVL - - - KNVKELCENLVKDDQVQVVVVCGKNTALKESLSALEAENGD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            310 ANFFEDRGAAIVVN----RHEEILESVTSLLADEDTLHRMKKNIKDLHLANSSEVIL 362
                                                               254 NGDKLKY-LGYVERIDELFRITDCMITKPGGITLTEATAIGVPVILYKPVP---GQEKEN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      71;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 407;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Transferase; Glycosyltransferase; Cell division; Cell wall;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Mycobacterium leprae.
Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      B757B73C092C53F9 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 137.5; DB 1;
Pred. No. 0.017;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Mismatches 112;
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                                                                                                                                                                                                                                                                                                                                                                                                  407
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Membrane; Peptidoglycan synthesis.
SEOUENCE 407 AA; 42422 MW; B75
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                49;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EMBL; AL022602; CAA18668.1; -.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
Brown D., Churcher C.M.,
Submitted (APR-1997) to t
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    20;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Tomb J.-F., White O., Kerlavage A.R., Clayton R.A., Sutton G.G., Fleischmann R.D., Ketchum K.A., Klenk H.-P., Gill S., Dougherty B.A., Nelson K., Quackenbush J., Zhou L., Kirkness E.F., Peterson S., Loftus B., Richardson D., Dodson R., Khalak H.G., Glodek A., McKenney K., Fitzgerald L.M. Lee N., Adams M.D., Hickey E.K., Berg D.E., Gocayne J.D., Utterback T.R., Peterson J.D., Kelley J.M., Cotton M.D., Weldman J.W., Fujlil C., Bowman C., Watthey L., Wallin E., Hayes W.S., Borodovsky M., Karp P.D., Smith H.O., Fraser C.M.,
 -EDTLHRMKKNIKDL 352
                         331 VVNAGGGLVVADDADLTPGLVARQVVRLFSDPAQLAAMTAAAARVGHRDAAHHVAKVALDL 390
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       124 TGRVIPTFNVMTDFCLHKIWVHE-----NVDKYY-----VATDYV-KEKLLEIGTHPS 170
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 64 IGKQFYRLFYYGVDKIYNKRKFNIYFKMGNKRLGELVDEHQPDIIINTFPMIVVPEYRRR 123
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          VNKSFFK----KIGSLFLQAKAAFKAK-----EILKKHQITHTISVGGFSAGPASFAS 111
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            10 LTANYGNGHVQVAKTLYEQCVRLGFQHVTVSNLYQ-----ESNPIVSEVTQYLYLKSFS 63
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      5 LTGGGTGGHLSIAKALAIELEKQGIEAIYLGSTYGQDKEWFENSPLFSE--RYFFNTQGV 62
                                                                                                                                 30-MAY-2000 (Rel. 39, Last sequence update)
30-MAY-2000 (Rel. 39, Last annotation update)
UDP-N-ACETYLGLUGOSAMINE-N-ACETYLMURAMYL-(PENTAPEPTIDE)
PYROPHOSPHORYL-UNDECAPRENOL N-ACETYLGLUGOSAMINE TRANSFERASE
(EC 2.4.1.-) (UNDECAPRENYL-PP-MURNAC-PENTAPEPTIDE-UDPGLUANC GLCNAC
                                                                                                                                                                                                                        Helicobacter pylori (Campylobacter pylori).
Bacteria; Proteobacteria; epsilon subdivision; Helicobacter group;
Helicobacter.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 complete genome sequence of the gastric pathogen Helicobacter
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Transferase; Glycosyltransferase; Cell division; Cell wall;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      6.9%; Score 136; DB 1; Length 353; 19.5%; Pred. No. 0.018;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Pred. No. 0.018;
; Mismatches 150; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              6D136CD92A180513 CRC64;
                                                                                            353 AA
313 FEDRGAAIVVNRHE----EILESVTSLLAD-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Membrane, Peptidoglycan synthesis.
SEQUENCE 353 AA; 39474 MW; 6D1
                                                                                                                                                                                                                                                                                                                             MEDLINE-97394467; PubMed-9252185;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 16;
                                                                                                                         Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EMBL; AE000621; AAD08196.1;
                                                                                                                                                                                                                                                                                                                / ATCC 700392;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Conservative
                                                                                            STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Similarity
                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A. STRAIN-26695 / ATC
                                                                                                                                                                                                                                                                       NCBI_TaxID=210;
                                                                                                                                                                                                                  MURG OR HP1155
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        HP1155;
                                                                                                                                                                                                     TRANSFERASE)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               78;
                                                                                                                      30-MAY-2000
                                                                                            MURG_HELPY
025770;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
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Matches 7
                                                                              MURG_HELPY
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STRAIN-JAL-1 / DSM 2661 / ATCC 43067;
STRAIN-JAL-1 / DSM 2661 / ATCC 43067;
MEDLINE-96337999; PubMed=8680807;
Bult C.J., White O., Olsen G.J., Zhou L., Fleischmann R.D.,
Sutton G.G., Blake J.A., Fitzgerald L.M., Clayton R.A., Gocayne J.D.,
Sutton G.G., Blake J.A., Fitzgerald L.M., Clayton R.A., Gocayne J.D.,
Scrlawage A.R., Dougherty B.A., Tomb J.F., Adams M.D., Reich C.I.,
Overbeek R., Kirkness E.F., Weinstock K.G., Merrick J.M., Glodek A.,
Scott J.L., Geoghagen N.S.M., Weidman J.F., Fuhrmann J.L., Nguyen D.,
Utterpack T.R., Kelley J.M., Peterson J.D., Sadow P.W., Hanna M.C.,
Cotton M.D., Roberts K.M., Hurst M.A., Kaine B.P., Borodovsky M.,
Klenk H.-P., Fraser C.M., Smith H.O., Woese C.R., Venter J.C.;
"Complete genome sequence of the methanogenic archaeon, Methanococcus
                                                                                                                                                                                                                                                                                                                                                                                                                             SRAGASSVWELCANGLPTI-FIPYPFASNNHQYYNVLEFEKENLCYVVPQNELLPKKLFE 311
--LYIHEQNAIKGSLNRYLSPKAKAVFSSYAFKDK---GNH-- 153
                                                                                                                                                                   154 -- VLTSYPVQNAF------FDFARTRTEIKHILFLGGSQGAKAINEFALLNAPK 199
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      200 LTKQGIK -- -- ITHICGPNS -- YEQVRFFYQELGLLDKIELFAFHNNITEIMHRADICV
                                                                                                                                                                                                                                          221 LCENLVKDDQVQVVVVCGKNTALKESLSALEAENG--DKLKVLGYVERIDELFRITDCMI
                                                                                                                                                                                                                                                                                                                                                                                    279 TKPGGITLTEATAIGVPVILYKPVP----GQEKENANFFEDRGAAIVVNRHE----EILE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ; Pred. No. 0.032;
63; Mismatches 114; Indels 126;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 484;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Archaea; Euryarchaeota; Methanococcales; Methanococcaceae; Methanococcus.
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                                                                                                NVKITGIPIRPQFEESMPVGPIYKKYNLSPNK---KVLLIMAGAHG-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              331 SVTSLLADED----TLHRMKKNIKDLHLANSSEVILEDIL 366
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              312 VIRKLNQKDDQGNKNLTTISNQLQQKIAKDGAKTITETIL 351
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ; DB 1;
0.032;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GVDKIYNK - - - - - - - - RKFN - + - - IYFKMGNKRLGELVDEH - -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   01-NOV-1997 (Rel. 35, Created)
01-NOV-1997 (Rel. 35, Last sequence update)
15-UL-1998 (Rel. 36, Last annotation update)
HYPOTHETICAL PROTEIN MJ1062.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           484 AA
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-!- SIMILARITY: STRONG, TO B.SUBTILIS SPSG.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 135;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Interpro; IPR000182; -.
Pfam; PF00583; Acetyltransf; 1.
Hypothetical protein SE00183; SE0018NCE 484 AA; 56693 MW; E
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EMBL; U67549; AAB99065.1; -.
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20.5%;
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Best Local Similarity 20.5'
Matches 78; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Methanococcus jannaschii
                             112 LLNKIP-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NCBI_TaxID=2190;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       YA62_METJA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  jannaschii.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FUNCTION: CELL WALL FORMATION. CATALYZES THE TRANSFER OF A GLCNAC SUBUNIT ON UNDECAPRENYL-PYROPHOSPHORYL-WURNAC-PENTAPEPTIDE (LIPID INTERNEDIATE I) TO FORM UNDECAPRENYL-PYROPHOSPHORYL-WURNAC-PENTAPEPTIDE)GLCNAC (LIPID INTERNEDIATE II) (BY SIMILARITY). PATHWAY: LAST STEP OF PEPTIDOGLYCAN BIOSYNTHESIS. SUBCELLULAR LOCATION: MEMBRANE ASSOCIATED (BY SIMILARITY). SIMILARITY: BELONGS TO THE MURG FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               282 LKKISKTHLNPLKEGYFIDAEHTDLHIGKGKFEIIEAITN-----IYNCKK-----I 328
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Smith D.R., Noonan B., Guild B.C., deJonge B.L., Carmel G., Tummino P.J., Caruso A., Uria-Nickelsen M., Mills D.M., Ives C., Gibson R., Merberg D., Mills S.D., Jiang Q., Taylor D.E., Vovis G.F.,
                                                                                                                                                                                                                                                                           ----PNKKVLLIMAGAHGVLKNVKELCENLVKDDQVQVVVVCGKNTALKESLSAL--EA 252
                                                                                                                                                                                                                                                                                                                                                                                                                          306
                                                281
QPDIIINTFPMIVVPEYRRRTGRVIPTFNVMTDFCLHKIWVHENVDKYYVATDYVKEKLL 163
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDLINE-99120557; PubMed-9923682; Aling B.L., Brown E.D., Doig P.C. Alm R.A., Ling L.-S.L., Moir D.#., King B.L., Brown E.D., Doig P.C. Smith D.R., Noonan B., Guild B.C., deJonge B.L., Carmel G.,
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01-OCT-2000 (Rel. 40, Last annotation update)
01-PA-ACETYLGHOCOSAMINE-N-ACETYLMURANIL-(PENTAPEPTIDE)
PYROPHOSPHORYL-UNDECAPRENOL N-ACETYLGHOCOSAMINE TRANSFERASE
(EC. 2.4.1.-) (UNDECAPRENUL-PP-MURNAC-PENTAPEPTIDE-UDPGLCNAC GLCNAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Helicobatter pylori J99 (Campylobacter pylori J99).
Bacteria; Proteobacteria; epsilon subdivision; Helicobacter group;
                                                                                                                                                                                                           FDNPNPSSNKYADIVVNAIVGSELKNRKYFDEENKTLYFYGPKYLILRNEFYKVKKEMLS
                                                                                                                                                                                                                                                                                                                        | :|: |: |: |: |: |: |: |: |: |: || RSKNKETKNILIAFGGSDPSNLTCKVLEELLSKDRDFNINVVLGPKFQYEDELNNLLKRY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   -----KENAN------FFEDRGAAIVVNRHE-EILESVTSLLADEDTLHRMKKNIKDLHL
                                                                                                                                                                                                                                                                                                                                                                                                                          ENGDKLKVLGYVERIDELFRITDCMITKPGGITLTEATAIGVP-VILYKPVPGQE----
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Membrane; Peptidoglycan synthesis.
SEQUENCE 353 AA; 39506 MW; 1773AD7E5C214EF9 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         353 AA
                                                                                                                                           EIGTHPSNVKITGIPI ------RPQFEESMPV-
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gastric pathogen Helicobacter pylori.";
Nature 397:176-180(1999)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        355 ANSSEVILEDIL-KESEMMTA 374
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (Rel. 39, Created)
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NCBI_TaxID=85963;
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Q9ZK59;
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-!- PATHWAY: LAST STEP OF PEPTIDOGLYCAN BIOSYNTHESIS.
-!- SUBCELLULAR LOCATION: MEMBRANE ASSOCIATED (BY SIMILARITY).
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                                                                                                                                                                                                                                                                                             252 VSRAGASSVWELCANGLPII-FIPYPFASNNHQYYNVLEFEKENLCYVVPQNELLPKKLF 310
                                                                                                                                                                                                                                                                                                                                        277
                                                                                                                                                                                                                                                                                                                                                              ITKPGGITLTEATAIGVPVILYKPVP----GQEKENANFFEDRGAAIVVNRHE----EIL 329
                                                                                                                                   IGKQFYR----LFYYGVDKIYNKRKFNIYFKMGNKRLGELVDEHQPDIIINTFPMIVVPE 119
                                                                                                                                                               VNKSFFKKIRSLF-----LQAKAAF------KAKEILKKHQITHTISVGGFSAGPA 1.07
                                                                                                    62
                                                                LTANYGNGHVQVAKTLYEQCVRLGFQHVTVSNLYQ-----ESNPIVSEVTQYLYLKSFS 63
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Mycobacterium tuberculosis.
Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;
Actinomycetales; Corynebacterineae; Mycobacteriaceae; Mycobacterium.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Cole S.T., Brosch R., Parkhill J., Garnier T., Churcher C., Harris Gordon S.V., Elgimeier K., Gas S., Barry C.E. III, Tekaia F., Badcock K., Basham D., Brown D., Chillingworth T., Connor R., Badries K., Devillin K., Feltwell T., Gentles S., Hamlin N., Holroyd Hornsby T., Jagels K., Krogh A., McLean J., Moule S., Murphy L., Oliver S., Seeger K., Skelton S., Squares S., Seeger K., Skelton S., Squares S., Squares R., Sulston J. Taylor K., Whitehead S., Barrell B.G., "Deciphering the biology of Mycobacterium tuberculosis from the Matter S., Squares S., Sarrell B.G.,"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GLCNAC
                                                                                                                                                                                                     120 YRRRIGRVIPTENVMIDECLHKIWVHE-----NVDKYY-----VAIDYV-KEKLLEIG
                                                                                                                                                                                                                                     SFASLLNKIP-----LYIHEONAIKGSLNRYLSPKAKAVFSSYAFKDK----G
                                                                                                                                                                                                                                                                       THPSNVKITGIPIRPQFEESMPVGPIYKKYNLSPNKKVLLIMAGAHG------VLKNVK
                                                                                                                                                                                                                                                                                                                                        ELCENLVKDDQVQVVVVCGKNTALKESLSALEAENG - - DKLKVLGYVERIDELFRITDCM
                                                                                                LTGGGTGGHLSIAKALAIELEKQGIEAIYLGSTYGODKEWFENSPLFSE--RYFFNTQGV
                                   98;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               30-MAY-2000 (Rel. 39, Last sequence update)
30-MAY-2000 (Rel. 39, Last annotation update)
UDP-N-ACETYLGLUCOSAMINE-N-ACETYLGRUNDERPEPTIDE)
PYROPHOSPHORYL-UNDECAPRENOL N-ACETYLGRUCOSAMINE TRANSFERASE
(EC. 2.4.1.-) (UNDECAPRENYL-PP-MURNAC-PENTAPEFTIDE-UDPGLUNDC
   Length 353;
                                   Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  330 ESVTSLLADED ----TLHRMKKNIKDLHLANSSEVILEDIL 366
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    6.8%; Score 134; DB 1; Lv
20.0%; Pred. No. 0.024;
iive 71; Mismatches 152;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       39, Created)
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                                     Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STANDARD;
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                       Similarity
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30-MAY-2000 (
30-MAY-2000 (
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SEQUENCE 1
        Query Match
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                                       Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                            146 ENVDKYYVATDYVKEKLLEIGTHPSNVKITGIPIRPQ---FEESMPVGPIYKKYNLSPNK 202
                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Bulkema W.J., Scappino L.A., Haselkorn R.;
Submitted (JAN-1996) to the EMBL/GenBank/DDBJ databases.
-!- FUNCTION: THE PROTEIN MAY PLAX A ROLE IN THE BIOSYNTHESIS OF
THE PROSTHETIC GROUP OF NITROGENASE (FEWO COFACTOR).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RVLLVFGGSQGAV-SLNRAVSGAAAD--LAAAGVCVLHAHGPQNVLELRRRAQGDPPYVA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LGYVERIDELFRITDCMITKPGGITLTEATAIGVPVILYKPVP···GQEKENANFFEDRG
                                                                                                                                                                                                                                                                                                                                               39;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      15-JUL-1999 (Rel. 38, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
NITROGENASE IRON-MOLYBDENUM COFACTOR BIOSYNTHESIS PROTEIN NIFE.
                                                                                                                                                                                                                                                                                                           DB 1; Length 410;
                                                                                                                                                                                             TubercuList; Rv2153c; -.
Transferase; Glycosyltransferase; Cell division; Cell wall;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1- SIMILARITY: BELONGS TO THE NIFD/NIFK/NIFE/NIFN FAMILY
                                                                                                                                                                                                                                                                                                       Score 128.5; DB 1; Length
Pred. No. 0.071;
5; Mismatches 124; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Anabaena sp. (strain PCC 7120).
Bacteria: Cyanobacteria; Nostocales; Nostocaceae; Nostoc.
NCBI_TaxID=103690;
                                                                                                                                                                                                                               Membrane; Peptidoglycan synthesis.
SEQUENCE 410 AA; 41860 MW; 96902AFE356FC30B CRC64;
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                                                                                                                                                                                                                                                                                   Query Match 6.5%; Scc
Best Local Similarity 19.9%; Pre
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(Rel. 38, Last seq
                                                                                                                                                                      EMBL; Z95388; CAB08640.1; -.
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15-JUL-1999
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NIFE_ANASP
ID NIFE_ANASP
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73 YYGVDKIYNKRKFNIYFKMGNKRLGELVDEHQPDIIINTFPMIVVPEYRRRTGRVIPTFN 132
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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                 This invention describes a novel protein (I) comprising identical or different catalytic domains of glloosyl transferases and which has processive activity (i.e. builds up oligosaccharide glycolipids by successive addition of glucose units). (I) can be used to produce 3-oligoglucosyl-1,2-dlacylglycerios useful as food emulsifiers, polymer modifiers or detergents. This sequence encodes a Bacillus subtilis glycosyl transferase catalytic domain which is used in the method of
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1080
                                                                                                                        Nucleic acids containing electron-transfer group, useful as labels in hybridization assays, e.g. for genotyping, allowing repeat analyses on
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Best Local Similarity 1.0%; Pre
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.2e-24;
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                                                                                                                                                                                                                         (CLIN+) CLINICAL MICRO SENSORS INC.
                                                                                              26-JUL-2000; 2000WO-US20476
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17-MAR-2000; 2000US-0190259
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Best Local Similarity
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                                                                                                                                   acggctttaaaaagaatctttgagtgcgcttgaagcggaaaatggtgacaaattaaaagtt 780
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17-MAR-2000; 2000US-0190259.
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Nucleic acids containing electron-transfer group, useful as labels in hybridization assays, e.g. for genotyping, allowing repeat analyses on a single surface
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ctgtgcgaaaaccttgtcaaggatgaccaagtgcaagtagttgtcgtgtgcgggaaaaat
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17-MAR-2000; 2000US-0190259.
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hes 295;
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1.0%; Pred. No. 9.2e-
Live 483; Mismatches
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                                                                                                                                                                                                                                                            Example 6; Page 128; 159pp; English.
                                                                                        (CLIN-) CLINICAL MICRO SENSORS INC.
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            26-JUL-2000; 2000WO-US20476.
                                         26-JUL-1999; 99US-0145695
17-MAR-2000; 2000US-0190259
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group, useful as labels in allowing repeat analyses on

Nucleic acids containing electron-transfer hybridization assays, e.g. for genotyping, a single surface

WPI; 2001-159728/16

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(CLIN-) CLINICAL MICRO SENSORS INC

Example 6; Page 127; 159pp; English,

The present invention relates to a composition comprising two nucleic acids each containing an electron-transfer group (ETM) having different redox potentials. The invention is used for electronic detection of nucleic acids, especially of substitutions (mismatches) and single-nucleotide polymorphisms, e.g. for genotyping,

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Length 938;

10.5%; Score 120.8; DB 22; Length. llarity 1.0%; Pred. No. 9.2e-24; Conservative 483; Mismatches 295; Indels

Similarity 8; Conserva

Query Match Best Local Si Matches 8;

Sequence 938 BP; 4 A; 144 C; 9 G; 5 T; 776 other;

monitoring gene expression.

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Electron-transfer group; ETM; mismatch; genotyping;

gene expression; ss

WO200107665-A2.

Synthetic.

01-FEB-2001,

(first entry)

24-APR-2001

Oligonucleotide D1876.

26-JUL-1999; 99US-0145695. 17-MAR-2000; 2000US-0190259. 26-JUL-2000; 2000WO-US20476

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Nucleic acids containing electron-transfer group, useful as labels in hybridization assays, e.g. for genotyping, allowing repeat analyses on
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AAF58254 standard; DNA; 936
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17-MAR-2000; 2000US-0190259.
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721 acggctttaaaagaatctttgagtgcgcttgaagcggaaaatggtgacaaattaaaagtt 780
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                                                                                   The present invention relates to a composition comprising two nucleic acids each containing an electron-transfer group (ETM) having different redox potentials. The invention is used for electronic detection of nucleic acids, especially of substitutions (mismatches) and single-nucleotide polymorphisms, e.g. for genotyping,
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                                                                                                                                                                                                                                                                                                                             10.4%; Score 120;
0.8%; Pred. No. 1.
                                              Example 6; Page 127; 159pp; English
                                                                                                                                                                                                                monitoring gene expression.
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  single surface
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                                                                                                                                                                       ETM; mismatch; genotyping;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 10.4%; Score 120; DB 22;
ilarity 0.8%; Pred. No. 1.5e-23;
Conservative 482; Mismatches 292;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Example 6; Page 127; 159pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (CLIN-) CLINICAL MICRO SENSORS INC
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17-MAR-2000; 2000US-0190259.
AAF58257 standard; DNA; 936
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ccgcaatttgaagaatccatgcctgttggcccgatatataaaaagtacaatctttcacca 600
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Length 936;
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                Pred. No. 1.5e-23;
2; Mismatches 292;
 DB 22;
 Score 120;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 936 BP; 5 A; 139 C; 10 G; 6 T; 776 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Pred. No. 1.5e-23;
12; Mismatches 292;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 120; DB 22;
                                                                                                                                                                                                                                                                                                          Example 6; Page 128; 159pp; English.
                                                                                                                                               (CLIN-) CLINICAL MICRO SENSORS INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match 10.4%; Sc
Best Local Similarity 0.8%; Pre
Matches 6; Conservative 482;
                                                             26-JUL-2000; 2000WO-US20476
                                                                                                            17-MAR-2000; 2000US-0190259
                                                                                               99US-0145695
                                                                                                                                                                                                         WPI; 2001-159728/16.
                                                                                                                                                                                                                                                                            single surface
WO200107665-A2.
                                                                                             26-JUL-1999;
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                                                                                                                                                                           Umek RM;
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group, useful as labels in allowing repeat analyses on
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0.8%; Pred. No. 1.5e-23;
Live 482; Mismatches 29
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Nucleic acids containing electron-transfer hybridization assays, e.g. for genotyping, a single surface
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                                                                                                                                                                                                                    BP
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17-MAR-2000;
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BP. AAV74438 standard; DNA; 12658 (first entry) 16-MAR-1999 AAV74438; AAV74438/C 

Computer readable medium; vaccine; S.aureus infection; immunodetection; cellulitis; eyelld infection; food poisoning; osteomyelitis; therapy; skin infection; surgical wound infection; scalded skin syndrome; toxic shock syndrome; ds.

Staphylococcus aureus contig SEQ ID #127

Staphylococcus aureus.

Location/Qualifiers
181...240
/\*tag= a
/note= these bases represent a line of missing text in
the sequence listing in the specification. They
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ghthese bases represent a line of missing text in the sequence listing in the specification. They are included to maintain the nucleotide numbering given in the specification for this DNA sequence. /note- "these bases represent a line of missing text in the sequence listing in the specification. They are included to maintain the nucleotide numbering given in the specification for this DNA sequence" "these bases represent a line of missing text in the sequence listing in the specification. They are included to maintain the nucleotide numbering given in the specification for this DNA sequence" "these bases represent a line of missing text in the sequence listing in the specification. They are included to maintain the nucleotide numbering given in the specification for this DNA sequence" are included to maintain the nucleotide numbering given in the specification for this DNA sequence" /note= "these bases represent a line of missing text in the sequence listing in the specification. They are included to maintain the nucleotide numbering given in the specification for this DNA sequence" 10981..11040 /\*tag= g /note= "these 7381..7440 /\*tag= e /note= "thes 9181..9240 /\*tag= f /note= "thes 5581..5640 /\*tag= d 3781..3840 misc\_feature misc feature misc\_feature misc\_feature misc\_feature

EP786519-A2 30-JUL-1997 97EP-0100117, 07-JAN-1997;

96US-0009861, 05-JAN-1996; (HUMA-) HUMAN GENOME SCI INC

Kunsch CA; Fannon MR, ЪЈ, Dillon Cho1 GH, SC, Rosen CA; Barash

WPI; 1997-374922/35.

Staphylococcus aureus in the production of Polynucleotide(s) and proteins derived from stored on computer readable medium and used anti-S.aureus vaccines

Claim 1; Page 692-699; 3271pp; English.

This sequence represents one of 5191 Staphylococcus aureus DNA sequences of the invention. The DNA sequences are recorded on a computer readable continuity preferably selected from a floppy or hard disk, random access menary (RAM), read-only memory (ROM) or CD-ROM. Homology searches using the S.aureus DNA sequences allows putative functions to be assigned so that protein-encoding or regulatory regions of commercial, therapeutic or industrial importance can be obtained. Specifically, sequences which are likely to encode antigens have been identified and these polypeptides can be used in a vaccine composition against S.aureus infection. The collypeptides can also be used in a kit for the immunodetection of S.aureus in a sample. S.aureus is implicated in numerous human diseases, including cellulitis, eyelid infections, food poisoning, osteomyelitis, syndrome, etc. Organisms transformed with the DNA sequences can be used for recombinant production of the polypeptides. The new DNA sequences of and their framemers) are useful as primers or probes for isolating computer readable medium.

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Search completed: June 29, 2001, 11:49:30 Job time: 5192 sec
                                                                            26-JUL-2000; 2000WO-US20476
                          WO200107665-A2
                                                                                                     26-JUL-1999;
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 Synthetic.
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                                      Length 12658;
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Sequence 12658 BP; 4296 A; 1711 C; 2283 G; 3942 T; 426 other;
                                                                Indels
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                                      DB 18;
                                                              0; Mismatches 369;
                                    Score 119.6; DB 1
Pred. No. 6.5e-23;
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                                    10.4%;
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                                                  Best Local Similarity 49.5
Matches 367; Conservative
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Nucleic acids containing electron-transfer group, useful as labels in hybridization assays, e.g. for genotyping, allowing repeat analyses on
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                                                                                  (CLIN-) CLINICAL MICRO SENSORS INC.
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99US-0145695
2000US-0190259
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Best Local Simil
Matches 11; C
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us-09-668-788-1.rst

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        GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
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Maximum Match 100%
Listing first 45 summaries
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Maximum DB seq length: 200000000
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190. gb\_estilo:\*
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209. gb\_gss1:\*
209. gb\_gss2:\*
209. gb\_g

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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AL447205 Parameciu
AL063921 Drosophil
AL063931 Brosophil
AL106896 Drosophil
BG591315 EST499157
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AZ66959 EST46151
AZ6787829 EST46151
AZ667366 ENTLC14TR
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ALO60428 DIOSOPHII
BF401494 UI-R-CAO-1
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HS_5529_A
sac60a08.
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ENTGC80TF
                                                                  AZ679140 ENTJO94TR
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AZ679140
GSS 14-DEC-2000
AZ679140
AZ679140.1 GI:11816286
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Entamoeba histolytica
Entamoeba histolytica
Eukaryota; Entamoebidae; Entamoeba.
1 (bases 1 to 893)
Loftus, B., Van Aken, S. and Fraser, C.
Determination of clone end sequences from Entamoeba histolytica
HM1: IMSS sheared DNA library
Unpublished (2000)
Contact: Brendan J Loftus
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AL098614 I
AW684087 I
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AZ550844
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AL071865
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AQ677419
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SUMMARIES
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AW787592
AI979696
PT007G23U
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AZ819893
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AZ891758
AZ684924
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64468988 47 11111
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TITLE
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Department of Eukaryotic Genomics
The Institute for Genomic Research
9712. Medical Center Dr., Rockville, MD 20850, USA
Tel: 301 838 0200
Fax:: 301 838 0200
Eax:: 301 838 0200
Clones are derived from the Entamoeba histolytica HM1:IMSS sheared
DNA ilbrary
Seq primer: M13-Reverse
Class: shotgun
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Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
Pterygota; Neoptera; Endopterygota; Diptera; Brachycera;
Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.
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High quality sequence stop: 757
Location/qualifiers
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Fax: 651-649-5058
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Submitted (02-JUN-1999) Genoscope - Centre National de Sequencage:

"Web : www. genoscope.cns.fr)

"Web : www. genoscope.cns.fr)

Determination of this BAC-end sequence was carried out as part of a collaboration with the Berkeley Drosophila Genome Project (BDGP).

The BDGP is constructing a physical map of the Drosophila melanogaster genome using these BACs. For further information please see http://www.fruitfly.org The BDGP Drosophila melanogaster BAC library was prepared by Kazutoyo Osoegawa and Aaron Mammosser in Pieter de Jong's laboratory in the Department of Cancer Genetics at the Roswell Park Cancer Institute in Buffalo, NY. The library is named RPCI-98 and was constructed by partial ECORI digestion of Drosophila DNA provided by the BDGP from the isogenic strain v2: cn bw sp, the same strain used for the BDGP's Pl and EST libraries. A more detailed description of the library and how to order individual BAC clones, the entire library, or fillers for hybridization from the BACPAC Resource Center can be found at http://bacpac.med.buffalo.edu/drosophila_bac.htm.
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/db_xrsf="taxon:7227"
/db_tref="taxon:7227"
/clone_libb="RPCI-98"
/clone="BACR22J10"
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ESTs from senescent nodules of Medicago truncatula
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Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            gaagoggaaaatggtgacaaattaaaagttotgggotatgtggagogcattgatgagota
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Email: vance004@marcon.tc.umn.edu
University of Minnesota name: M27.3210e TIGR sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 44.4; DB 143; Length
Pred. No. 0.29;
0; Mismatches 141; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 411 Borlaug Hall, 1991 Upper Buford Circle, Tel: 612 625 5715
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MTKBA54TK More information is available at: http://chrysle.tam.vedu/medicago Seq primer: SKmod (CTA gAA CTA gtg gAT CC). Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Unpublished (2000)
Contact: Carroll P. Vance
Department of Agronomy and Plant Genetics
University of Minnesota
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /organism="Medicago truncatula"
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                                                                                          BE999232.1 GI:10699508
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   3.98;
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Matches 145; Conservative
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DEFINITION

ACCESSION

VERSION KEYWORDS

ORGANISM

SOURCE

AUTHORS TITLE

JOURNAL

COMMENT

FEATURES

REFERENCE

AW787593/C

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/organism="Zea mays"
/cultivar="W23"
/dultivar="W23"
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/dultivar="W23"
/dultivar="W23"
/dultivar="W23"
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same as 707 (SK)"
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/lab_host="DH10B"
/dev_staqe="fully-grown"
/dev_forentiated maize tissues from an active Mutator plant.
Tissue ratio is 4:2:1:1:1:1 (tassel, kernel, silk, husk,
root, leaf). Unidirectionally cloned. New library number
given to library 707 for additional sequencing."
AW78/592 595 bp mRNA EST 16-MAY-2000
945011D04.X1 945 - Mixed adult tissues from Walbot lab, same as 707
AW78/592
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                                                                                                                                                                                                                    Eukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta, Spermatophyta, Magnoliophyta, Liliopsida, Poales, Poaceae, PACC clade, Panicoideae, Andropogoneae, Zea.

1 (bases 1 to 595)
Walbot, V.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 408 TCTAAATGATTATATTGCTGGACAGGAAGCTGGCAATGTCCCCTACGTTGTTGAAAATGG 349
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        528 AGTICAGGIGAAAGGCITIGITACAAAGAIGGAAGAAIGIATGGGIGCITGIGATIGIAT 469
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       468 CATTACAAAGGCAGGACCTGGTACAATTGCAGAGGCAATGATCGTGGCTTACCAATTAT 409
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                                                                                                                                                                                                                                                                                                                                               Maize ESTs from various cDNA libraries sequenced at Stanford
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                                                                                                                                                                                                                                                                                                                                                                 University
Unpublished (1999)
Contact: Walbot V
Department of Biological Sciences
Stanford University
855 California Ave, Palo Alto, CA 94304, USA
Tel: 650 725 8221
Fax: 650 725 8221
Email: walbot@stanford.edu
Plate: 945011 row: D column: 04.
Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DB 120;
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Pred. No. 0.36;
0; Mismatches 113;
                                                                                                                               GI:7844370
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Best Local Similarity 49.8%;
Matches 112; Conservative
                                                                                                                               AW787592.1
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Zea mays
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                                                                                                                               AW787593 548 bp mRNA EST 16-MAY-2000
945011D04.X2 945 - Mixed adult tissues from Walbot lab, same as 707
(SK) Zea mays CDNA, mRNA sequence.
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Vector: pGAD10; Site_1: EcorR: cDNA library from fully
differentiated maize tissues from an active Mutator plant.
Tissue ratio is 4:2:1:1:1:1 (tassel, kernel, silk, husk,
root, leaf). Unidirectionally cloned. New library number
given to library 707 157 t
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( bases 1 to 548)
Walbot,V.

Maize ESTs from various cDNA libraries sequenced at Stanford
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /db_xref=raxon:4077"
/db_xref=raxon:4077"
/clone_lib="945___Mixed adult tissues from Walbot lab, same as 707 (SK)"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               531 AGTTCAGGTGAAAGGCTTTGTTACAAAGATGGAAGAATGTATGGGTGCTTGTGTTGTAT 472
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             891 tctgtacaaacccgtgcctggccaggaaaaagaaaatgcaaacttcttgaagaccgcgg 950
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                           321 CCTTATGTGGTAAACAATGGAGCTGGTGTCTTCACTCGCAGTCCTAAAGAAA 372
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 44.2; DB 120; Length
Pred. No. 0.35;
0; Mismatches 113; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           855 California Ave, Palo Alto, CA 94304, USA Tel: 650 723 2227
Fax: 650 728 8221
Exail: walbot@stanford.edu
Plate: 945011 row: D column: 04.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Contact: Walbot V
Department of Biological Sciences
Stanford University
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/organism="Zea mays"
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                                                                                                                                                                                                                                                                    AW787593.1 GI:7844371
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Best Local Similarity 49.8%;
Matches 112; Conservative
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Unpublished (1999)
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Zea mays
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Gaps

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BASE COUNT ORIGIN

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RESULT 5 AW787592/C

951

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ORGANISM

SOURCE

AUTHORS TITLE

REFERENCE

JOURNAL

COMMENT

FEATURES

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Direct Submission
Submitted (02-JUN-1999) Genoscope - Centre National de Sequencage :
BP 191 91006 EVRY cedex - FRANCE (B-mail : segrefégenoscope.cns.fr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CNS0039G 1101 bp DNA GSS 03-JUN-1999
Drosophila melanogaster genome survey sequence TET3 end of BAC #
BACR08K10 of RPCI-98 library from Drosophila melanogaster (fruit
Dessen, P., Zagulski, M., Gromadka, R., Plattner, H., Kissmehl, R., Meyer, E., Betermier, M., Schultz, J.E., Linder, J., Pearlman, R.E., Kung, C., Forney, J., Satir, B., Van Houten, J.L., Keller, A.M., Froissard, M., Sperling, L. and Cohen, J.
Paramecium genome survey: a pilot project
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             105 gcatgtaacagtttctaatttgtaccaagagtcaaatccgattgtttcagaggtaactca 164
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.

[] (bases 1 to 1101)

Genoscope.
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                                                                                                                                                      Random sequencing of the Paramecium macronuclear genome Unpublished
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  84; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /organism="Paramecium tetraurelia"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 43.6; DB 258;
Pred. No. 0.48;
0; Mismatches 84;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 172
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         fly), genomic survey sequence. AL063921
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /db_xref="taxon:5888"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /strain="stock d4-2"
                                                                                                                        3 (bases 1 to 438)
Gromadka, R. and Zagulski, M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      fruit fly.
Drosophila melanogaster
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Best Local Similarity 52.8'
Matches 94; Conservative
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EcoRI; Site_2: XhoI; 3-4 days old root tissue from Walbot
                                          Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACC clade; Panicoldeae; Andropogoneae; Zea.
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20114709

2 (bases 1 to 438)
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Eukaryota; Alveolata; Ciliophora; Oligohymenophorea; Peniculida;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    771 attaaaagttctgggctatgtggagcgcattgatgagctatttcggatcacagattgcat 830
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        831 gattaccaagcccggcggcattactttgacagaagccacagccattggagtgcctgtcat 890
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PT007G23U 438 bp DNA GSS 02-NOV-2000 Paramecium tetraurelia sequence M07D12u of the end of plasmid PT007G23, genomic survey sequence.
                                                                                                                                                                                                                                                                                                                                                                                             /organism="Zea mays"
/cultivar="wa2"
/db xref="taxon:4577"
/clone_lib="614 - root cDNA library from Walbot Lab"
/dssue_type="root"
/dev_stage="3-4" days old"
/lab_host="xtolrR"
                                                                                                                    Walbbt,V.
Maize ESTs from various cDNA libraries sequenced at Stanford
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Pred. No. 0.36;
0; Mismatches 113; Indels 0;
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Department of Biological Sciences
Stanfornia Ave, Palo Alto, CA 94304, USA
Tel: 650 723 227
Fax: 650 725 8221
Email: walbotéstanford.edu
Plate: 614045 row: D column: 09.
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Keller, A.M. and Cohen, J.
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Matches 112; Conservative
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Determination of this BAC-end sequence was carried out as part of a collaboration with the Berkeley Drosophila Genome Project (BDGP). The BDGP is constructing a physical map of the Drosophila melanogaster genome using these BACs. For further information please see http://www.fruitfly.org The BDGP Drosophila melanogaster BAC library was prepared by Kazutoyo Osogawa and Aaron Mammoser in Pieter de Jong's laboratory in the Department of Cancer Genetics at the Roswall Park Cancer Institute in Buffalo, NY. The library is named RPCI-98 and was constructed by partial EcoRI digestion of Drosophila DNA provided by the BDGP from the isogenic strain y2; cn bw By, the same strain used for the BDGP's Pl and EST libraries. A more detailed description of the library and how to order individual BAC clones, the entire library, or filters for hybridization from the BACPAC Resource Center can be found at http://Dacpac.med.buffalo.edu/drosophila_bac.htm.
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Drosophila melanogaster genome survey sequence TET3 end of BAC #
BACR08M12 of RPCI-98 library from Drosophila melanogaster (fruit fly), genomic survey sequence.
AL063931.1 GI:4941700
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/clone_lib="RPCI-98"
/clone="BACR08K10"
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- Web : www.genoscope.cns.fr

- Web : www.genoscope.cns.fr)

Determination of this BAC-end sequence was carried out as part of
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The BDGP is constructing a physical map of the Drosophila
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Cancer Genetics at the Roswell Park Cancer Institute in Buffalo,
NY. The library is named RPCI-98 and was constructed by partial
ECORI digestion of Drosophila DNA provided by the BDGP from the
isogenic strain y2; on bw sp, the same strain used for the BDGP's
Pl and EST libraries. A more detailed description of the library
and how to order individual BAC clones, the entire library, or
filters for hybridization from the BACPAC Resource Center can be
found at http://bacpac.med.buffalo.edu/drosophila_bac.htm.
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                                                                                                                                                           Direct Submission
Submitted (02-JUN-1999) Genoscope - Centre National de Sequencage :
BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr
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Drosophila melanogaster genome survey sequence T7 end of BAC
BACN16D22 of DrosBAC library from Drosophila melanogaster (fruit
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                355
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Plasmid Drosophila melanogaster
Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
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                     Pterygota; Neoptera; Endopterygota; Diptera; Brachycera;
Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.
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/db_xref="taxon:727"
/clone_lib="RPCI-98"
/clone="BACKOBM12"
/note="end : TET3"
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ilarity 35.7%; Pred. No. 0.7;
Conservative 43; Mismatches 135;
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                                                                                                                                     Genoscope
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/organism="Solanum tuberosum"
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(EDGP) -
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                                                             Submitsed (13-JUL-1999) Genoscope - Centre National de Sequencage : Submitted (13-JUL-1999) Genoscope - Centre National de Sequencage : BP 191 91006 EVYR cedex - FRANCE (E-mail : seqref@genoscope.cns.fr - Web : www.genoscope.cns.fr)
Determination of this BAC-end sequence was carried out as part of a collaboration with the European Drosophila Genome Project (EDGP) - http://www.edgp.ebi.ac.uk - . This Drosophila melanogaster BAC ibrary (Dros BAC) was made by Alain Billaud at CEPH (Centre d'Etude du Polymorphisme Humain) with funding provided by a MRC project grant. The DNA was prepared from embryos by Alain Bucheton and Genevieve Payan. It has been constructed in the vector
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Submitted (23-UL-1999) Genoscope - Centre National de Sequencage :
BP 191 91006 EVRY cedex - FRANCE (E-mail : segref@genoscope.cns.fr - Web : www.genoscope.cns.fr)
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ALI08352
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Pterygota; Neoptera; Endopterygota; Diptera; Brachycera;
Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.
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                                                                                                                                                                                                                                                                                                        /organism="Drosophila melanogaster"
/plasmid="pBeloBAC11"
/db_xref="taxon:7227"
/clone_llb="prosBAC"
/clone="BACN16D22"
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Pred. No. 0.79;
2; Mismatches 121; I
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31.2%; Pred
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EST499157 P. infestans-challenged leaf Solanum tuberosum cDNA clone
BPLIG16 5' sequence, mRNA sequence.
BG591315, GI:13609455
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Determination of this BAC-end sequence was carried out as part of a collaboration with the European Drosophila Genome Project (EDGP) - http://www.edgp.ebi.ac.uk -. This Drosophila melanogaster BAC library (Gros BAC) was made by Alain Billaud at CEPH (Centre d'Etude du Polymorphisme Humain) with funding provided by a MRC project grant. The DNA was prepared from embryos by Alain Bucheton and Genevieve Payan. It has been constructed in the vector
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Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Asteridae; euasterids I; Solanales; Solanaceae; Solanum.

(bases 1 to 687)
Zhang,P., Hernandez,M., Tornqvist,C.-E, Wirtz,U., Loukoianov,A.,
Rangel,P., Haberlach,G.T., Cho,J., Chiemingo,A., Bougri,O., Buell
,C.R., Ronning,C.M., Helgeson,J. and Baker,B.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         35 ARGTAARTIKTAAAAAAAAAATAATAATAAAATBAATAATATWATWWTIMTITIRAAWTTT 676
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/organism="Drosophila melanogaster"
/plasmid="pBeloBAC11"
/db_xref="taxon:7227"
/clone_lib="DrosBAC"
/clone="BACN37G19"
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Unpublished (1200)
Contact: Cathy Ronning
The Institute for Genomic Research
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102 c 257 g
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                                                                                                                                                                                                              /note="Vector: pBluescript SK(-); Site_1: EcoRI; Site_2: XhoI; WhoLe plants were challenged with 450,000 sporangia/ml P. infestans US-1(US 940501) in Biotron (Madison, Wisconsin). Leaf tissue was collected at 1, 2, 5, 12, and 24 hours post-challenge and frozen in liquid nitrogen immediately upon removal. Kennebec plants showed no signs of HR. Katahdin plants (susceptible to P. infestans US-1) were used as controls and showed infection. NOTE: We cannot exclude the possibility that thus sequence is actually derived from Phytophthora rather than potato."
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Clones are derived from the Entamoeba histolytica HM1:IMSS sheared
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A2678871 852 bp DNA GSS 14-DEC-2000
ENTKE39TR_Entamoeba histolytica Sheared DNA Entamoeba histolytica
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0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 687;
                                                       /clone="BPLISC16"
/clone_lib="P. infestans-challenged leaf"
/tsue_type="leaf"
/dev_stage="6 week old"
/lab_host="SOLR"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Indels
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/strain="HM1:IMSS"
/db_xref="taxon:5759"
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3.7%; Score 42.6; DE
Best Local Similarity 54.9%; Pred. No. 1;
Matches 84; Conservative 0; Mismatches
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Eukaryota; Entamoebidae; Entamoeba.
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High quality sequence stop: 788.
Location/Qualifiers
/cultivar="Kennebec"
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Seq primer: M13-Reverse
Class: shotgun
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Direct Submission

Direct Submission

Submitted (12-JUN-1999) Genoscope - Centre National de Sequencage :

BP 191 91006 EVRY cedex - FRANCE (E-mail : seqrefégenoscope.cns.fr - Web) : www.genoscope.cns.fr - Getermination of this BAC-end sequence was carried out as part of Determination of this BAC-end sequence was carried out as part of a collaboration with the Berkeley Drosophila Genome Project (BDGP).

The BDGP is constructing a physical map of the Drosophila melanogaster genome using these BACs. For further information please see http://www.fruitfly.org The BDGP Drosophila melanogaster BAC library was prepared by Kazutoyo Osoegawa and Aaron Mammoser in Pieter de Jong's laboratory in the Department of Cancer Genetics at the Roswell Park Cancer Gonetics at the Roswell Park Cancer Institute in Buffalo, NY. The library is named RPCI-98 and was constructed by partial EcoRI digestion of Drosophila DNA provided by the BDGP from the Laogenic strain y2; on bw sp, the same strain used for the BDGP's PI and BSI libraries. A more detailed description of the library and how to order individual BAC clones, the entire library, or filters for hybridization from the BACPAC Resource Center can be
/clone_lib="Entamoeba histolytica Sheared DNA"
/note="Vector: pHOS1; Site_1: Bst I; Constructed at The Institute for Genomic Research (TIGR), Rockville, MD.
Genomic DNA isolated from broth cultures of E. histolytica using a method described by Clark and Diamond, L.S. (1993) Entamoeba histolytica: a method for isolate identification. Exp. Parasitol.
77:450.). The DNA was mechanically sheared to give a tight size distribution (-2 kb). The v + i method used for the library construction is described in detail in Smith, H.O. and Venter, J.C. (Making small insert libraries for whole genome shotgun sequencing projects. In Genome Sequencing: A Practical Approach, eds. M. Vaudin and B. Barell, Oxford University Press, 1999)."
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             281 aaagattýggggaacttgtcgatgaacatcagccgatattattaatacatttccga 340
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Drosophila melanogaster

Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Inse
Pteryjota; Neoptera; Endopterygota; Diptera; Brachycera;
Muscomorpha; Enhydroidea; Drosophilidae; Drosophila.

(bases 1 to 1001)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            3.7%; Score 42.4; DB 247; Length 852; 51.6%; Pred. No. 1.2; 91; Indels 0;
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AL066953
AL066953.1 GI:4945517
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Best Local Similarity 51.6
Matches 97; Conservative
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Alcala,J., Vrebalov,J., White,R., Matern,A.L., Vision,T., Holt,I.E.
Liang,F., Opton,J., Ronning,C.M., Craven,M.B., Fujii,C.Y., Bowman,C.L., Nierman,W., Fraser,C.M., Venter,J.C., Martin,G.B., Tanksley,S.D. and Glovannoni,J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Lycopersicon esculentum
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Asteridae; euasterids I; Solanales; Solanaceae; Solanum;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AI487829 526 bp mRNA EST 29-JUN-1999 EST246151 tomato ovary, TAMU Lycopersicon esculentum cDNA clone cLED13F18, mRNA sequence.
                                                                                                                                                                                                                                                                                                    120 taatttgtaccaagagtcaaatccgaftgtttcagaggtaactcaatacctttatttaaa 179
                                                                                                                                                                                                                                                                                                                           180 aagetteteaategggaaacagttttategtttgttttattaeggagttgaeaaateta 239
                                                                                                                                                                                                                                                                                                                                                                                                    240 taataaacgtaaattcaatatttactttaaaatgggtaa-taaaagattgggcgaacttg 298
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1; Gaps
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Location/Qualifiers
1. .1001
                                                                                                                                                                                                                                DB 219; Length 1001;
                                                                                                                                                       331 others
                                                                                                                                                                                                                                                                      Indels
                                                     /organism="Drosophila melanogaster"
/db_xref="taxon:7227"
/clone_lib="RRCI-98"
/clone="BACR15H24"
/note="end : TET3"
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                                                                                                                                                                                                                            Query Match 3.7%; Score 42; DB 219; I Best Local Similarity 26.5%; Pred. No. 1.6; Matches 71; Conservative 83; Mismatches 113;
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/clone="clED18718"
/clone_lib="tomato ovary, TAMU"
/tissue_type="carpe1"
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Contact: David Frisch
Clemson University Genomics Institute
Clemson University
100 Jordan Hall, Clemson, SC 29634, USA
Tel: 864 656 4366
Fax: 864 656 4293
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /organism="Lycopersicon/cultivar="TA496"
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Location/Qualifiers
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AI487829.1 GI:4383200
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Search completed: June 29, 2001, 10:55:47 Job time: 5010 sec

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/dev_stage="5 days pre-anthesis to 5 days post-anthesis"
/lab_host="XL1-Blue MRF"
/note="Vector: pBlueScript SK(-); Site_1: ECOR1; Site_2:
/hote="Vector: pBlueScript EST Library. OligodT-primed and directionally cloned cDNA in vector Lamda 2AP II with 5' and 3' ends located at the EcoRI and XhoI sites,
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                                                                                                                                                                                                                                                                    Length 526;
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                                                                                                         June 29, 2001, 09:56:28 ; Search time 119.12 Seconds (without alignments) 1786.972 Million cell updates/sec
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/cgn2_6/ptodata/1/ina/5B_COMB.seq:*
/cgn2_6/ptodata/1/ina/6A_COMB.seq:*
/cgn2_6/ptodata/1/ina/6B_COMB.seq:*
/cgn2_6/ptodata/1/ina/PCTUS.COMB.seq:*
/cgn2_6/ptodata/1/ina/PCTUS.COMB.seq:*
GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
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US-07-991-867-25-96

US-08-107-755A-25

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US-08-107-755A-1

US-08-107-108-1

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US-08-617-860B-3
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Maximum Match 100%
Listing first 45 summaries
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Maximum DB seq length: 200000000
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Perfect score:
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Sequence 266, App
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Sequence 224, Appl
Sequence 173, Appl
Sequence 173, App
Sequence 292, Appl
Sequence 343, Appl
Sequence 5, Appl1
Sequence 2, Appl1
Sequence 2, Appl1
Sequence 2, Appl1
Sequence 9, Appl1
Sequence 9, Appl1
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          US-08-480-604A-9
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6669
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5435
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## ALIGNMENTS

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ZIP: 22313-0299
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING:SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/232,463
                                                                                                            APPLICANT: CHECKATION:
APPLICANT: CHECK, F.
APPLICANT: SCHEIFLINGER, F.
APPLICANT: FALKNER, F. G.
TITLE OF INVENTION: RECOMBINANT FOWLPOX VI
NUMBER OF SEQUENCES: 52
CORRESPONDENCE ADDRESS:
ADDRESSEE: Roley & Lardner
STREET: 1800 Diagonal Road, Suite 500
CITY: Alexandria
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PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/07/935,313
FILING DATE:
Sequence 14, Application US/08232463 Patent No. 5670367
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LENGTH: 7218 base pairs
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STRANDEDNESS: single
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                                                                     419 ataaaatttgggttcacgaaaacgtggataaatattatgtggcgacagattacgtgaagg 478
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APPLICANT: HERNELL, OLLE
APPLICANT: HERNELL, OLLE
APPLICANT: HERNELL, OLLE
APPLICANT: HANSON, KARIN
APPLICANT: HANSON, LENNART
APPLICANT: TORNELL, JAN
APPLICANT: TORNELL, JAN
APPLICANT: TORNELL, JAN
APPLICANT: TORNELL, JAN
APPLICANT: TORNELON: IT AND USE THEREOF
INVENTION: IT AND USE THEREOF
CORRESPONDENCE: 24
CORRESPONDENCE ADDRESS:
ADDRESSEE: BROWDY AND NEIMARK
                                       ;
 Length 7218;
Query Match
4.3%; Score 49; DB 1; Length 721
Best Local Similarity 2.7%; Pred. No. 0.00047;
Matches 10; Conservative 216; Mismatches 151; Indels
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARRE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/078,090
FILING DATE: 19930618
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICATION NUMBER: WO PCT/DK91/00233 FILING DATE: 19-AUG-1991 ATTORNEY/AGENT INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 3, Application US/08078090 Patent No. 5739407
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Pred. No. 0.19;
0; Mismatches 102; Indels 0;
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..6886, 7991..8521, 9440..9445)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AUDRESSEE: Dechert Price & Rhoads
STREET: 4000 Bell Atlantic Tower, 1717 Arch Stre
STATE: PA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SOFTWARE: Fast5EQ for Windows Version 2.0 CURRENT APPLICATION DATA: APPLICATION NUMBER: US/08/988,251
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R: GM10094
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Patent No. 6013497
GENERAL INFORMATION:
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REGISTRATION NUMBER: 28,354
REFERENCE/POCKET NUMBER: GM
TELECOMMUNICATION INFORMATION:
TELEPHONE: 215-994-2252
REFERENCE/DOCKET NUMBER: BE TELECOMMUNICATION: TELEPHONE: (202)628-5197
                                                                                                                                                                                                     TOPOLOGY: linear MOLECULE TYPE: DNA (genomic)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: Wallis, Nicola G.
TITLE OF INVENTION: MurE
NUMBER OF SEQUENCES: 6
CORRESPONDENCE ADDRESS:
ADDRESSEE: Dechert Price &
                                                                                                                                                                                                                                                                                                                                                                                          3.5%;
                                                                        TELEX: 248633
INFORMATION FOR SEQ ID NO: 3: SEQUENCE CHARACTERISTICS: LENGTH: 10607 base pairs TYPE: nucleic acid
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MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
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                                                         (202)737-3528
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Best Local Similarity 49.8
Matches 101; Conservative
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PRIOR APPLICATION DATA:
APPLICATION NUMBER:
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                                                                                                                                                                 TYPE: nuclei
STRANDEDNESS:
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ZIP: 19103
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; LOCATION:
US-08-078-090-3
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NAME/KEY:
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                                                                                                                                                                                                   Gaps
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                                                                                                                                                                      DB 3; Length 2600;
                                                                                                                                                                   Score 38.2; DB 3; Length 2 Pred. No. 0.3; 0; Mismatches 213; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: Wallis, Nicola
APPLICANT: Shilling, Lisa
APPLICANT: Sabelerowski, Susan
TITLE OF INVENTION: MurE
FILE REFERENCE: GM10094-D1
CORRENT APPLICATION NUMBER: US/09/386,048
CORRENT APPLICATION NUMBER: US/09/386,048
CORRENT FILING DATE: 1999-08-30
EARLIER APPLICATION NUMBER: US 60/059,956
EARLIER FILING DATE: 1997-12-10
EARLIER FILING DATE: 1997-09-25
NUMBER OF SEQ ID NOS: 6
SOFTWARE: FASTSEQ FOR WINDOWS Version 4.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 1, Application US/09386048 Patent No. 6103507
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ; TYPE: DNA
; ORGANISM: Staphylococcus aureus
US-09-386-048-1
                                                                                                                                                                     3.3%;
                         INFORMATION FOR SEQ ID NO: 1
SEQUENCE CHARACTERISTICS:
LENGTH: 2600 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
                                                                                                                                                                                Best Local Similarity 46.9
Matches 201; Conservative
TELEFAX: 215-994-2222
                                                                                                       linear
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-09-386-048-1/c
                                                                                                       TOPOLOGY:
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Best Local S
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              TELEX:
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                                                                                                                                                                                                                                                                                                                                                                                     314 AAACTAGACAAATGTTTTTACAAATACTATGGACTTAATAAGTTAATTTATTGATA 255
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          304 gaacatcagcccgatattattattaatacatttccgatgatcgtcgtgccggaatacaga 363
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       254 PAAGAAAAGCCAGATTTAATATTATTAACGTTTCCTACACCAGTTATGTGGGTACTAACT 195
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              194 GAGCAATTTAACATTAATATTCCAGTTGCTACAGTGATGACAGACTATCGTTACATAAA 135
                                                                                                                                                                                                                                                                      aaacgtaaattcaatatttactttaaaatgggtaataaaagattgggcgaacttgtcgat 303
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  364 cgccgaactggaagagtcattcctaccttcaacgttatgactgatttttgtcttcataaa 423
                                                 Gaps
                                                                                     10 aataaaagagtattaattttgactgcaaattacggaaatggacatgtgcaggtagccaaa 69
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GENERAL INFORMATION:

APPLICANT: Whoriskey, Susan K.
APPLICANT: Quinn, Cheryl L.
APPLICANT: Tao, Niajun
APPLICANT: Tao, Niajun
APPLICANT: Schimmel, Paul R.
TITLE OF INVENTION: Synthetase Genes, Tester Strains and Assays
NUMBER OF SEQUENCES:
CORRESPONDENCE ADDRESS:
                                                 15;
    Length 2600;
Score 38.2; DB 4; Length 2
Pred. No. 0.3;
0; Mismatches 213; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STREE: Lexington Brook, Smith & Reynolds, P.C. CITY: Lexington STREE: Massach:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PatentIn Release #1.0, Version #1.30
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CURRENT APELICATION DATA:
APPLICATION NUMBER: US/08/415,593
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 39, Application US/08415593
Patent No. 5912140
Patent No. 5912140 5776726
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      I: Floppy disk
IBM PC compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             REGISTRATION NUMBER: 22,592, RECISTRATION NUMBER: CP. TELECOMMUNICATION INFORMATION: ELPEPHONE: 617-861-6240
  3.3%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ATTORNEY/AGENT INFORMATION:
NAME: Brook, David E.
Query Match 3.3°
Best Local Similarity 46.9°
Matches 201; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FILING DATE:
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER: IBM PC OPERATING SYSTEM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         424 atttgggtt 432
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 134 AACTGGATT 126
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      266 ttaaaatgggtaataaaagattgggcgaacttgtcgatgaacatcagcccgatattatta 325
                                                                                                                                                                                                                                                                                                                    146 ttgtttcagaggtaactcaatacctttatttaaaaagcttctcaatcgggaaacagtttt 205
                                                                                                                                                                                                                                           Length 2128;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GENERAL INFORMATION:
APPLICANT: MORI, Tetsuya
APPLICANT: TAMAMOTO, KOZO
APPLICANT: OHTA, TSUNETARA
TITLE OF INVENTION: RECOMBINANT DNA AND TRANSFORMANT
TITLE OF INVENTION: CONTAINING THE SAME
NUMBER OF SEQUENCES: 20
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/828,511
FILING DATE: 31 MAR-1997
                                                                                                                                                                                                                                                                              95;
                                                                                                                                                                                                                                  Ouery Match
3.1%; Score 36; DB 2;
Best Local Similarity 49.5%; Pred. No. 1.1;
Matches 93; Conservative 0; Mismatches 99
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ADDRESSEE: BROWDY AND NEIMARK
STREET: 419 Seventh Street, N.W., Suite 300
CITY: Washington
STATE: D.C.
COUWTRY: USA
IP: 20004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICATION NUMBER: JP 342237/1993
FILING DATE: 15-DEC-1993
ATTORNEY/AGENT INFORMATION:
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PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/355,245
FILING DATE: 09-DEC-199-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         REFERENCE/DOCKET NUMBER: MORI=39
TELECOMOUNICATION INFORMATION:
TELEPHONE: 202-628-5197
TELEFAX: 202-737-3528
                                                                                                                          TOPOLOGY: linear

MOLECULE TYPE: other nucleic acid

US-08-415-593-39
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Patent No. 5731193
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     REGISTRATION NUMBER: 37,971
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         INFORMATION FOR SEQ ID NO: 1: SEQUENCE CHARACTERISTICS:
               INFORMATION FOR SEQ ID NO: 3
SEQUENCE CHARACTERISTICS:
LENGTH: 2128 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
617-862-9540
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   YUN, Allen C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FILING DATE: 09-DEC APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1927 TTATTAAA 1920
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FILING DATE: 31 CLASSIFICATION:
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US-08-828-511-1
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80 ATAGCCTTTTAATTTTTAATTCTTTTATCATTCTTTGCAATAATAAAACATTAAC 139
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                                                                                                                                                                                                                                                                                                                   20 AAAATCIATTTTCAAAAAAGTIGCTCTAAGAATATAGTTATCAAGTTAAGTAAAATGTCA 79
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TITLE OF INVENTION: Secondinant Pneumoycstis Aminoacyl tRNA TITLE OF INVENTION: Synthetase Genes, Tester Strains and Assays NUMBER OF SEQUENCES: 46 CORRESPONDENCE ADDRESS: ADDRESSE: Hamilton, Brook, Smith & Reynolds, P.C. STREET: Two Militia Drive CITY: Lexington STREET: Massachusetts
                                                                                                                                                                                           3.0%; Score 34.6; DB 1; Length 486; 51.6%; Pred. No. 1.5; tive 0; Mismatches 74; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ZIP: 02173
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPPERTING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN Release #1.0, Version #1.30
CURRENT APPLICATION NUMBER: US/08/415,593
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       258 tatttactttaaaatgggtaataaaagattggg 290
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: Whoriskey, Susan K.
APPLICANT: Quinn, Cheryl L.
APPLICANT: Tao, Niajun
APPLICANT: Politis-Virk, Karen I.
APPLICANT: Sohimmel, Paul R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 40, Application US/08415593
Patent No. 5912140
Patent No. 5912140 5776726
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ATTORNEY/AGENT INFORMATION:
NAME: BIOOK, DAVID E.
REGISTRATION NUMBER: 22,592
REFERENCE/DOCKET NUMBER: CPI9.
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-861-6240
TELEPHONE: 617-861-6240
LENGTH: 486 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LENGTH: 1991 base pairs
                                                                                                                                                                                        Query Match 3.0
Best Local Similarity 51.6
Matches 79; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TELEFAX: 617-862-9540 INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TYPE: nucleic acid
STRANDEDNESS: double
                                                                                             MOLECULE TYPE: CDNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     linear
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; LOCATION:
.US-08-415-593-40
                                                                                                                   US-08-828-511-1
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Gaps

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1919 GITATITITAAATATGCAAAAACTATAAAAACTAATGTAGTITAACCAACTITITICIA 1978
                                                                                                                                                                                                                                                                                                                                                     200 agttttatogtttgttttattaoggagttgacaaaatotataaataaaogtaaattoaata 259
                                                                                                                                                                                                                                                                                                             320 ttattattaatacatttccgatgatcgtcgtgccggaatacagacgccgaactggaagag 379
                                                                                                                                                                                                                                  260 tttactttaaaaatgggtaataaaagattgggcgaacttgtcgatgaacatcagcccgata 319
                                                                                                                                                                                                                                                                                                                                                                                                                                380 tcattcctaccttcaacgttatgactgatttttgtcttcataaaatttgggttcacgaa 438
                                                                            Length 5852;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           3.0%; Score 34; DB 1; Length 1000;
                                                                          Score 34.2; DB 1; Length 5
Pred. No. 5.3;
0; Mismatches 128; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TITLE OF INVENTION: METHOD TO DIAGNOSE HEREDITARY TITLE OF INVENTION: HEMOCHROMATOSIS NUMBER OF SEQUENCES: 124
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             E: MORRISON & FOERSTER
2000 Pennsylvania Ave. N.W., Suite 5500
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SOFTWARE: Patentin Release #1.0, Version #1.30 CUBRENT APPLICATION DATA:
PAPLICATION NOMBER: US/08/599,252 FILING DATE: 09-PEB-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          9053-0001.21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDÍUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 96, Application US/08599252 Patent No. 5705343 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: MURASHIGE, KATE H.
REGISTRATION NUMBER: 29,959
REFERENCE/DOCKET NUMBER: 9053-
TELECOMMUNICATION INFORMATION:
TELEPAN: (202) 887-1500
TELEFAN: (202) 887-0763
TELEFX: 90-4030
INFORMATION FOR SEQ ID NO: 96:
SEQUENCE CHRARATICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: FEDER, JOHN N.
APPLICANT: GRIRKE, ANDREAS
APPLICANT: KIMMEL, BRUCE E.
APPLICANT: THOMAS, WINSTON J.
APPLICANT: WOLFF, ROGER K.
TITLE OF INVENTION: METHOD TO
TITLE OF INVENTION: HEMOCHROMA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DENNIS T.
                                                                        3.0%;
ilarity 46.4%;
Conservative
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nucleic acid
EDNESS: single
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy of
  2378..5038
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                                                                                               Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CITY: Washington
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STREET: 20
; LOCATION:
US-07-867-106-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ; TOPOLOGY:
US-08-599-252-96
                                                                                                              111;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COUNTRY:
                                                                        Query Match
Best Local Si
Matches 111;
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                                                                                                            146 ttgtttcagaggtaactcaatacctttatttaaaaagcttctcaatcgggaaacagtttt 205
                                                                                                                                                                                       206 atcgtttgttttattacggagttgacaaaatctataataacgtaaattcaatatttact 265
                                                                                                                                                                                                                                                                 266 ttaaaatgggtaataaaagattgggggaacttgtcgatgaacatcagcccgatattatta 325
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ADDRESSEE: Woodcock Washburn Kurtz Mackiewicz & No. 5389526ris
STREET: One Liberty Place 46th Floor
CITY: Philadelphia
                                                                          ö
                               Score 34.4; DB 2; Length 1991;
Pred. No. 3;
0; Mismatches 96; Indels 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                               US-07-867106-2
Sequence 2, Application US/07867106
Sequence 2, Application US/07867106
Settle No. 5389526
SETTLE No. 5389526
SETTLE OF INVENTION: APPLICANT: Williams, Keith L
STITLE OF INVENTION: Improved Plasmid Vectors for Cellular
TITLE OF INVENTION: Slime Moulds of the Genus Dictyostellum
NUMBER OF SEQUENCES: 19
CORRESPONDENCE ADDRESS:
ADDRESSEE: Woodcock Washburn Kurtz Mackiewicz & No. 538952
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
PPLICATION NUMBER: US/07/867,106
FILING DATE: 19920625
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICALLOND DATE: 19920625
FILING DATE: 19920625
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/AU90/00530
APPLICATION NUMBER: PCT/AU90/00530
APPLICATION NUMBER: PCT/AU90/00530
APPLICATION NUMBER: PCT/AU90/00530
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           REFERENCE/DOCKET NUMBER: RICE-0002
TELECOMMUNICATION INFORMATION:
TELEPHONE: 215-568-3100
TELEPAX: 215-568-3439
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 iEDUCH.
LENGTH: 5852 Dac.
TYPE: NUCLEIC ACID
STRANDEDNESS: single
TOPOLOGY: linear
TOPOLOGY: DAN (genomic)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NAME: Feeney, Joanne Longo
REGISTRATION NUMBER: 35,134
                               3.0%;
ilarity 48.9%;
Conservative (
                                                 Similarity
                                                                                                                                                                                                                                                                                                                                                                                    1797 TTATTAAA 1790
                                                                                                                                                                                                                                                                                                                                                ttaataca 333
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CDS
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                                   Query Match
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Matches
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                                                                                                  METHOD TO DIAGNOSE HEREDITARY HEMOCHROMAŢOSIS
                                                                                                                                                                                                                                                                                                                                                                                                                                       2000 Pennsylvania Ave. N.W., Suite 5500
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               90;
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); Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/599,252
FILING DATE: 09-FEB-1996
ATTORNEY/AGENT INFORMATION:
NAME: MURASHIGE, KATE H.
REGISTRATION NUMBER: 29,959
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICATION NUMBER: PCT/US96/06583 FILING DATE:
                                                                                                                                                                                                      Sequence 96, Application PC/TUS9606583 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STAIL.
COUNTRY: USA
ZIP: 2006-1888
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
MEDIUM TYPE: Floppy disk
TYPE: Floppy disk
PC COMPATIBLE
                                                                                                                                                                                                                                                                                                                                                                                                                       MORRISON & FOERSTER
                                                                                                                                                                                                                                      APPLICANT: DRAYNA, DENNIS T.
APPLICANT: FEDER, JOHN N.
APPLICANT: GNIRKE, ANDREAS
APPLICANT: KIMMEL, BRUCE E.
APPLICANT: THOMAS, WINSTON J.
APPLICANT: WOLFF, ROGER K.
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TELEPHONE: (202) 887-1500
TELEFA: (202) 887-0763
TELEX: 90-4030
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Best Local Similarity 49.4%;
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TITLE OF INVENTION: HEN
NUMBER OF SEQUENCES: 12
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   nucleic acid
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PCT-US96-06583-96
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                        Gaps
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                      90; Indels
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APPLICANT: KIMMEL, BRUCE E.
APPLICANT: THOMAS, WINSTON J.
APPLICANT: WOLFF, ROGER K.
TITLE OF INVENTION: METHOD TO DIAGNOSE HEREDITARY
TITLE OF INVENTION: HEMOCHROMATOSIS
NUMBER OF SEQUENCES: 124
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              E: MORRISON & FOERSTER
2000 Pennsylvania Ave. N.W., Suite 5500
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Patentin Release #1.0, Version #1.30
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0; Mismatches
                    0; Mismatches
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PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/599,252
FILING DATE: 09-FEB-1996
ATTORNEY/AGENT INFORMATION:
NAME: MURASHIGE, KATE H.
REGISTRATION NUMBER: 29,959
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SOFTWARE: Patentin Release #1.0, v
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US96/06352
                                                                                                                                                                                                                                                                                                                             Sequence 96, Application PC/TUS9606352 GENERAL INFORMATION:
     Pred.
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2IP: 20006-1888
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   REFERENCE/DOCKET NUMBER: 9053
TELECOMUNICATION INCORMATION:
TELEPHONE: (202) 887-1500
TELERA: 90-4030
INFORMATION FOR SEQ ID NO: 96: SEQUENCE CHARACTERISTICS:
LENGTH: 1000 base pairs
                                                                                                                                                                                                                                                                                                                                                             APPLICANT: DRAYNA, DENNIS T. APPLICANT: FEDER, JOHN N.
   49.48;
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                    88; Conservative
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Best Local Similarity 49.4
Matches 88; Conservative
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EDNESS: single
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ADDRESSEE: MORRISON
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Best Local Similarity
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STATE:
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Indels
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CITY: STATE:

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                                                                                                               APPLICANT: Moyer, Richard W.
APPLICANT: Hall, Richard L.
APPLICANT: Hall, Richard L.
APPLICANT: Gruidl, Michael E.
TITLE OF INVENTION: No. 5721352el Entomopoxvirus Expression System
NUMBER OF SEQUENCES: 40
CORRESPONDENCE ADDRESS:
ADDRESSEE: David R. Saliwanchik
STREET: 2421 N.W. 41st Street, Suite A-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: Moyer, Richard W.
APPLICANT: Hall, Richard L.
APPLICANT: Gruidl, Michael E.
TITLE OF INVENTION: No. 5935777el Entomopoxvirus Expression System
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Pred. No. 3.8;
0; Mismatches 67; Indels 0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1 0
5, Application US/08107755A
5721352
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          324 tattaatacatttccgatgat 344
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TELEFAX: (904) 372-5800
INPORMATION FOR SEQ ID NO: 25.
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match 2.9%;
Best Local Similarity 52.5%;
Matches 74; Conservative
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STATE: Florida
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                                                                                                                                                                                                                                                            APPLICANT: Moyer, Richard W.
APPLICANT: Hall, Richard L.
APPLICANT: Hall, Michael E.
APPLICANT: Gruid! Michael E.
TITLE OF INVENTION: No. 5476781el Entomopoxvirus Expression System
NUMBER OF SEQUENCES: 66
CORRESPONDENCE ADDRESS:
ADDRESSEE: David R. Saliwanchik
STREET: 2421 N.W. 41st Street, Suite A-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DB 1; Length 1395;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COUNTRY: USA
ZUP: 32606
ZUP: 32606
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/991,867B
FILING DATE: 12-DEC-1992
CLASSIFICATION: 435
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2.9%; Score 33.8; DF
Best Local Similarity 52.5%; Pred. No. 3.8;
Matches 74; Conservative 0; Mismatches
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RECISTRATION NUMBER: 31,794
REFERENCE/DOCKET NUMBER: UF114.C3
TELECOMMUNICATION INFORMATION:
TELEPHONE: 904-375-8100
TELEFAX: 904-375-800
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICATION NUMBER: US 07/827,685 FILING DATE: 30-JAN-1992 PRIOR APPLICATION DATA: APPLICATION NUMBER: US 07/657,584 FILING DATE: 19-FEB-1991 ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRIOR APPLICATION DATA:
APPLICATION NUMBER: WO 92/14818
FILING DATE: 12-FEB-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/827,68
                                                                                                                                                     Sequence 25, Application US/07991867B Patent No. 5476781 GENERAL INFORMATION:
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SEQUENCE CHARACTERISTICS:
LENGTH: 1395 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ; MOLECULE TYPE: DNA (genomic) US-07-991-867B-25
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STRANDEDNESS: doub
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                                                                                                                      US-07-991-867B-25/C
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US-08-107-755A-25/c
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204 ttatcgtttgttttattacggagttgacaaaatctataaaacgtaaattcaatattta 263
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 6768;
                                                                                                                                                                                                                                                    COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPUTER: DatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: 19-AUG-1993
CLASSIFICATION DATA:
APPLICATION NUMBER: US 07/827,658
FILING DATE: 30-AMN-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/657,584
FILING DATE: 19-FEB-1991
ATTORNEY/AGENT INFORMATION:
NAME: SAILWANCHIK, DAVIG R.
REGISTRATION NUMBER: 31,794
REFERENCE/DOCKET NUMBER: 31,794
REFERENCE/DOCKET NUMBER: 3175-8100
TELEPHONE: (904) 375-8100
TELEFRAX: (904) 375-8100
TELEFRAX: (904) 375-5800
INPORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                i, DB 1;
7.2;
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                                                                                                                       ADDRESSEE: David R. Saliwanchik
STREET: 2421 N.W. 41st Street, Suite A-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ORIGINAL SOURCE:
ORGANISM: Amsacta moorei entomopoxvirus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    complement (2239..2475)
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TYPE: nucleic acid
STRANDEDNESS: double
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2502..2987
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3080..6091
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1474..2151
                                                                                                                                                                               CITY: Gainesville
STATE: Florida
COUNTRY: U.S.A.
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Matches 74; Conserva
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LOCATION:
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FEATURE:
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NAME/KEY:
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FEATURE:
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; LOCATION:
US-08-107-755A-1
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                                                                                                                                                                                                                                                                                                                                                           SOFTWARE: Patentin Release #1.0, Version #1.25 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          67;
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                                                        SEE: Gerard H. Bencen: 2421 N.W. 41st Street, Suite A-1 Gainesville
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match 2.9%; Score 33.8; D
Best Local Similarity 52.5%; Pred. No. 3.8;
Matches 74; Conservative 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CLASSIFICATION: 435
CLASSIFICATION 1435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/991,867
FILING DATE: 07-0EC-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/107,755
FILING DATE: 19-AUG-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: WO 92/14818
FILING DATE: 12-FEB-1992
PRIOR APPLICATION NUMBER: WO 92/14818
FILING DATE: 30-JAN-1992
PRIOR APPLICATION NUMBER: US 07/827,685
FILING DATE: 30-JAN-1992
PRIOR APPLICATION NUMBER: US 78/87
A
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                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICATION NUMBER: US/08/544,332
                                                                                                                                                                                                                                                    COMPUTER: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
OSCHWARE: PatentIn Policy
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Patent No. 5721352
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    REGISTRATION NUMBER: 35,746
REFERENCE/DOCKET NUMBER: UF1
ELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                324 tattaatacatttccgatgat 344
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MOLECULE TYPE: DNA (genomic)
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APPLICANT: Moyer, Richard W.
APPLICANT: Hall, Richard L.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           INFORMATION FOR SEQ ID NO: 25: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TELEPHONE: 904-375-8100
TELEFAX: 904-372-5800
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LENGTH: 1395 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NAME: Bencen, Gerard H. REGISTRATION NUMBER: 35
   NUMBER OF SEQUENCES: 77
                               CORRESPONDENCE ADDRESS:
                                                                                                                                                                               COUNTRY: USA ZIP: 32606
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 unknown
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                                                                                                                                                                                                                                                                                                                                                                                                                                                            FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RESULT 15
US-08-107-755A-1/C
                                                           ADDRESSEE:
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Search completed: June 29, 2001, 11:46:43 Job time: 6615 sec

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June 29, 2001, 08:56:07; Search time 35.83 Seconds (without alignments) 646.340 Million cell updates/sec
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1970
1 MNTNKRVLILTANYGNGHVQ.......BDILKESENMTAKQKAKVLS 382
GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                                                                              Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                             412676 seqs, 60623988 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                                                  - protein search, using sw model
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Gapop 10.0 , Gapext 0.5
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Maximum DB seq length: 2000000000
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Perfect score:
Sequence:
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                                                                                  OM protein
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/ SIDS8/gogdata/geneseq/genesegp/AA1980.DAT:\*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

Description	B. subtilis glycos	Amino acid sequenc	Arabidopsis thalia	Arabidopsis thalia	Monogalactosyldiac	Amino acid sequenc	Amino acid sequenc	Amino acid sequenc	Arabidopsis thalia	WO9905287 Sed ID 1	Neisseria gonorrhe
SUMMARIES	AAY33444	AAB19039	AAG42414	AAG42413	AAW41148	AAB19040	AAB19041	AAB19042	AAG42415	AAW92952	AAY74401
DB	20	21	21	21	19	21	21	21	21	50	21
% Query Watch Length DB	382	522	492	551	422	525	533	468	404	468	355
% Query Match	100.0	16.5	15.7	15.7	15.5	15.4	15.3	14.9	14.6	5.8	5.8
Score	1970	326	309.5	309.5	305.5	303.5	301.5	293	287.5	114.5	113.5
Result No.	н	7	m	4	ß	9	7	80	6	10	11

x 6 6 6 6	Arabidopsis thalia Mutant thermostabl Mutant thermostabl Mutant thermostabl Mutant thermostabl Mutant thermostabl Nelseria meningit SPS protein. Zea Mutant thermostabl Taf DNA polymerase	Nucleolar/endosoma vgaB streptogramin Catalpa speciosa s Merozite apical-en Merozite apical-en S. cerevisiae L947 S. cerevisiae L947 Leishmania brazili M. jannaschii MJO8 M. jannaschii MJO8 An Escherichia col S. aureus firsy pro Heilothis armigera Arabidopsis thalia
AAW98240 AAW30198 AAW38266 AAW92950 AAW92950 AAG31533 AAG31531 AAG50592 AAG50591		AAW96299 AAY32265 AAY32265 AAY3265 AAW24575 AAW64392 AAW64384 AAY52023 AAY52023 AAY52033 AAY52053 AAY54652 AAW92993 AAY58277
113 113 118 118 118 121 121 121 121 121 121 121		2011 111 113 113 113 113 113 113 113 113
993 1068 1068 478 469 503 572 572	009 009 009 009 009 009 009 009 009 009	1411 6688 1254 1254 473 1198 1634 1634 367 367 3103
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112.5 112.5 112.5 110 110 110 110	100 100 100 100 100 100 100 100 100	100 100 100 100 100 100 100 100 100 100
12 14 14 17 18 19 20 20	252 252 252 253 253 253 253 253 253 253	0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0

## ALIGNMENTS

444 444 444 AAY33444 standard; Protein; 382 AA. AAX33444; 13-DEC-1999 (first entry)  B. subtlis glycosyl transferase catalytic domain. Catalytic domain; glycosyl transferase; processive activity; detergent; oligosaccharide glycolipid; 3-oligoglucosyl-1,2-diacylglycerol; food emulsifier; polymer modifier; glycosyl transferase. Bacillus subtliis. DE19819958-A1.
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                        This invention describes a novel protein (I) comprising identical or different catalytic domains of glycosyl transferases and which has processive activity (i.e. builds up oligosaccharide glycolipids by successive addition of glucose units). (I) can be used to produce a 3-oligoglucosyl-1, 2-diacylglycerols useful as food emulsifiers, polymer modifiers or detergents. This sequence represents a Bacillus subtilis glycosyl transferase catalytic domain which is used in the method of
                                                                                                                                                                                                                                                                                                                                                                                    360
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TALKESLSALEAENGDKLKVLGYVERIDELFRITDCMITKPGGITLITEATAIGVPVILYK 300
                                                                                                                                                                                                                                                                                  SFSIGKQFYRLFYYGVDKIYNKRKFNIYFKMGNKRLGELVDEHQPDIIINTFPMIVVPEY 120
                                                                                                                                                                                                                                                                                               RRRIGRVIPTFNVMTDFCLHKIWVHENVDKYYVATDYVKEKLLEIGTHPSNVKITGIPIR 180
                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                               Monogalactosyl-diacylglycerol synthase; MGDG synthase; Toxoplasma; apicomplex parasite; herbicide; antiparasitic; Plasmodium; Eimeria; acquired immune deficiency syndrome; coccidiosis.
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                                                                                                                                                                                 Length 382;
                                                                                                                                                                                                           Indels
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                                                                                                                                                                               100.0%; Score 1970; DB 20;
100.0%; Pred. No. 1.6e-180;
iive 0; Mismatches 0;
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                                                                                                                                                                                                 Similarity
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                                                                                                                                               382 AA;
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                                                                                                                      the invention.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        pathway;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         KRVLILTANYGNGHVQVAKTLYEQCVRLGFQ-----HVTVSNLYQESN--PIVSEVTQ
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                                                                                                                                                   Use of monogalactosyl diacylglycerol synthase for identifying its specific inhibitors, potentially useful as antiparasitic agents ar herbicides
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; Pred. No. 1.2e-22;
80; Mismatches 162;
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Joyard J,
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25.3%;
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Best Local Similarity 25.38
Matches 98; Conservative
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        Block M,
                                                                                WPI; 2000-602227/57
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        Marechal E,
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Protein identification; signal transduction pathway; metabolic pathway; hybridisation assay; genetic mapping; gene expression control; promoter; termination sequence.
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99US-0135124.
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99US-0136021.
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99US-0139452.
99US-0139453.
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99US-0123548.
99US-0125788.
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99US-0138094
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25-MAR-1999;
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01-APR-1999;
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                                                                                                      202 dhtpwpfnglprsynflvkhg---tlwkmtyygtsprivhgsnfaatstfiarelagglm 258
                                                           102 EHQPDIIINTFPMI--VVPEYRRTG--RVIPTFNVMTDF-CLHKIWVHENVDKYYVATD 156
                                                                                                                                                                                                                                                                                                                                                           267 IDELFRITDCMITKPGGITLTEATAIGVPVILYKPVPGQEKENANFFEDRGAAIVVNRHE 326
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    V--LKNVKELCENLVKDDQV----QVVVVCGKNTALKESLSALEAENGDKLKVLGYVER
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reasing lipid production in transformed host
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The present sequence represents a monogalactosyl-diacylglycerol (M3DG) synthase. MGDG is present in all plastids tested and is essential for cell survival, but is not present in other membrane structures, or in animal cells, and so represents a specific target. MGDG synthase or a plastid membrane isolated from plants is used to select and screen for specific inhibitors of MGDG synthase. These inhibitors are suitable as active agents against apicomplex parasities or as herbicides. The inhibitors are used as antiparasitic agents, especially against plasmodium, Toxoplasma (particularly in patients with acquired immune deficiency syndrome) or Eimeria (coccidiosis in cattle or poultry), and
Amino acid sequence of monogalactosyl-diacylglycerol (MGDG) synthase.
                                                                          Monogalactosyl-diacylglycerol synthase; MGDG synthase; Toxoplasma; aplcomplex parasite; herbicide; antiparasitic; Plasmodlum; Elmeria; acquired immune deficiency syndrome; coccidiosis.
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                                                                                          5 KRVLILTANYGNGH----VQVAKTLYEQCVRLGFQHVTVSNLYQESNPIVSEVTQYLYKS
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                                                                        33;
                                                    Length 525;
                                                  15.4%; Score 303.5; DB 21; Length 25.7%; Pred. No. 1.7e-20; ive 77; Mismatches 179; Indels
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Matches 100; Conservative
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as herbicides
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            Synthase. Middle present in all plastids tested and is essential for cell survival, but is not present in other membrane structures, or in animal cells, and so represents a specific target. MGDG synthase or a plastid membrane isolated from plants is used to select and screen for specific inhibitors of MGDG synthase. These inhibitors are suitable as active agents against aplicomplex parasites or as herbicides. The inhibitors are used as antiparasitic agents, especially against plasmodium, Toxoplasma (particularly in patients with acquired immune deficiency syndrome) or Elmeria (coccidiosis in cattle or poultry), and
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monogalactosyl-diacylglycerol
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                                                                                                                                                                                                                                                                                                                                              DB 21;
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Arabidopsis thaliana.
                                                             EP1033405-A2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       14;
                                                                                                                                                                                                                        The present sequence represents a monogalactosyl-diacylglycerol (MGDG) synthase. MGDG is present in all plastids tested and is essential for cells invival, but is not present in other membrane structures, or in animal cells, and so represents a specific target. MGDG synthase or a plastid membrane isolated from plants is used to select and screen for specific inhibitors of MGDG synthase. These inhibitors are sultable as active agents against apicomplex parasities or as herbicides. The inhibitors are used as antiparasitic agents, especially against plasmodium, Toxoplasma (particularly in patients with acquired immune deficiency syndrome) or Elmeria (coccidiosis in cattle or poultry), and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Protein identification; signal transduction pathway; metabolic pathway; hybridisation assay; genetic mapping; gene expression control; promoter; termination sequence.
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69 knvlllmsdtggghrasaeairdafkiefgdkyrvivkdvwkeytgwplndmersykfmv 128
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                                                                                                               Use of monogalactosyl diacylglycerol synthase for identifying its specific inhibitors, potentially useful as antiparasitic agents and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             14.9%; Score 293; DB 21; Length 468; 25.1%; Pred. No. 1.5e-19; Live 86; Mismatches 172; Indels 3:
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                                     Block M, Joyard J,
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                                     Marechal E,
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Pred. No. 3.9e-19;
3; Mismatches 169; Indels
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23.6%; Pred
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Best Local Similarity 23.6
Matches 97; Conservative
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Query Match
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                                                                                                                                                            Plant; flavonoid 5-transglycosylation activity; 5TG; variety; colour.
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Gene encoding a plant flavonoid 5-transglycosylation enzyme used to transform plants for improvement of plant coloration
                                                                                                                                                                                                                                                                                                                           Saito K, Tanaka Y;
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                                                                   AAW92952 standard; Protein; 468
                                                                                                                                                                                                                                                                                                                        Gong 2, Kusumi T, Mizutani M,
Yamazaki M;
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N-PSDB; AAX02831.
                                                                                                                                                                                                                                                                                                   (SUNR ) SUNTORY LTD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       468 AA;
                                                                                                                                                                                   Petunia hybrida
                                                                                                                                                                                                         WO9905287-A1
                                                                                                                                                                                                                                                     16-JUL-1998;
                                                                                                                                                                                                                                                                            25-JUL-1997;
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                                                                                          AAW92952;
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Matches
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                                                          AAW92952
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represent novel Neisseria meningitis and N. gonorrheae polynucleotides and polypeptides. AZZ4537 to AZZ5576 and AAZ54616 to AAZ55473 represent PCR primers used in the exemplification of the present invention. The polypeptides, the polynucleotides, antibodies and compositions of the invention can be used as vaccines, as diagnostic reagents, and as manufacture of medicaments for treating or preventing infection due to Neisserial bacteria (e.g. meningitis and septicaemia), to detect the presence of Neisseria bacteria, or to raise antibodies. They may also be used to screen for agonists or antagonists, which may themselves may also be used as antibacterial agents. The polynucleotides of the invention may also be used in gene therapy protocols.
                                                                                                                                                                                                                                                                                                                                                                                                                                                            antigen; vaccine;
meningitis; septicaemia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Ξ
Mora M;
Scarselli
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAZ53015 to AAZ54536, AAZ54577 to AAZ54615, and AAY74253 to AAY75941
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Novel Neisserial polypeptides predicted to be useful antigens for vaccines and diagnostics
                                                                                                                                                                                                                                                                                                                                                                                                     Neisseria gonorrheae ORF 087 protein sequence SEQ ID NO:278
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Masignani V,
Scalato E, S
                                                                                                                                                                                                                                                                                                                                                                                                                                                  Neisseria meningitidis; Neisseria gonorrheae; antigenic; diagnosis; immunogenic; infection; antibacterial; gene therapy.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Hickey E,
Ratti G,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Claim 2; Page 277-278; 1453pp; English.
                                                                                                                                                                                                                                                  AAY74401 standard; Protein; 355 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Fraser C, Galeotti C, Grandi G,
Petersen J, Pizza M, Rappuoli R,
Tettelin H, Venter JC;
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98US-0103796.
99US-0121528.
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                                                                            339 EDTLHRMKKNIK 350
                                                                                                                              437
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Neisseria gonorrheae
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WPI; 2000-062150/05.
                                                                                                                           426 gekgeelrknak
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09-OCT-1998;
25-FEB-1999;
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02-SEP-1998;
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Length 355;

21;

Score 113.5; DB Pred. No. 0.016;

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Best Local
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  18;
                                                                                                                                                                                                                                                                                                                                                                                                      Helicobacter infection; gastroduodenal disease; gastritis;
                                                                     222 CENLVKDDQVQVVVVCGKNTALKESLSALEAEN---GDKLKVLGYVERIDELFRITDCMI 278
                                                                                                                                                                                      IGKQFYRLFYYGVDKIYNKRKFNIYFKMGN--KRLGELVDEHQPDIIIN----TFP--- 113
                                                                                               -----MIVVPEYRRTG---RVIPTFNVMTDFCLHKIWVHENVDKYYVATDYVKEKLL 163
                                                                                                                                      221
                                                                                                                                                        -----glvgnpvradi-snlpv-paerfqgregrlkilvvggslgadvlnktvpqa 203
                                                                                                                                                                                                                279 TKPGGITLTEATAIGVPVILYKPVP----GQEKENANFFEDRGAAIVVNRHEEILESVTS 334
                                                                                                                                                                                                                              This sequence represents a Helicobacter pylori GHPO protein of the invention. The polypeptides can be used for preventing or treating Helicobacter infections, and gastroduodenal diseases associated with
   Gaps
                   RVLILTANYGNGHVQVAKTLYEQCVRLCFQHVTVSNLYQESNPIVSE--VTQYLYLKSFS 63
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 products
                            EIGTHPSNVKITGIPIRPQFEESMPVGPIYKKYNLSPNKKVLLI--MAGAHGVLKNVKEL
                                                                                                                  111 aakllgvpiviheqnavaglsnrhlsrwakrvlyafpkafsheg-------
  85;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              New isolated Helicobacter polynucleotides - used to develop for the diagnosis, prevention and treatment of Helicobacter infections and gastrointestinal diseases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Tomb J;
 Mismatches 158; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Oomen RP,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MERIEUX ORAVAX PASTEUR MERIEUX SERUMS.
                                                                                                                                                                                                                                                       335 LLADEDTLHRMK-----KNIKDLHLANSSEVILE 363
                                                                                                                                                                                                                                                                  :| :|:| | :|:| | 318 ilg---slnrekclkwaenartlalphsaddvae 348
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Claim 8; Page 200-204; 2054pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Kleanthous H, Miller C,
                                                                                                                                                                                                                                                                                                                        AAW98240 standard; Protein; 993 AA
 71;
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97US-0833457.
97US-0881227.
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 Conservative
                                                                                                                                                                                                                                                                                                                                                                                                     GHPO protein; Helicol
peptic ulcer disease
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24-JUN-1997;
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80;
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these infections, including acute, chronic, and atrophic gastritis, and peptic ulcer diseases, e.g. gastric and duodenal ulcers. They can also be used for the production of antibodies. The products can also be used for detection and diagnosis.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                200
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                                                                                                                                                                                                                                                                                                                          101 riilwekdtksgekngikdikeqsifireiplmtertsfiingvervvvnglhrspgvif 160
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    151
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              253 ENGDKLKVLGYVERIDE---LFRITDCMITKPGGITLTEATAIGVPVILYKP-----VP 303
                                                                                                                                                                                                                                                                                 ----GFQHVTVSNLYQESNPIV 50
                                                                                                                                                                                                                                                                                                                                                                     51 SEVTQYLYLKSFSIGKQFYRLFYYGVDKIYNKRKFNIYFKMG-----NKR----- 95
                                                                                                                                                                                                                                                                                                                                                                                                     96 - LGELVDEHOPDIIINTFPMIVVPEYRRRTGRVIPTFNVMTDFCLHKIWVHENVDKY - - -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           152 YVATDYVKEKLLEIGTHPSNV-----KITGIPIRPOFEESM-----PVGPIYKKYNLSP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    243 fasldangrmefdlkdpggkvillagkkltsrkikelkenhlewveypmdillnrhlaep
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NKKVLLIMAGAHGVLKNVKELCEN---LVKDDQVQVVVV-----CGKNTALKESLSALEA
                                                                                                                                                                                  5.7%; Score 112.5; DB 19; Length 993; 20.5%; Pred. No. 0.091; ive 70; Mismatches 154; Indels 145;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SPS; (fructose-6-phosphate; UDP-glucose; sucrose regulation;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ADEDILH ---- RMKKNIKD -- LHLANSSEVILEDILKESEMMTA 374
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ||:| || :|:||| || 473 ane--lhsglvkmqktikdklttmsgafdslmphdlvnskmits 514
                                                                                                                                                                                                                                                                              6 RVLILTANYGNGHVQVAKTLYEQCVRL-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sucrose phosphate synthase from corn.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Ā
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// 1abel = 4K
// note=" tryptic"
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ID AAR20198 standard; Protein; 1068
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/label= A8
/note="tryptic"
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/label= B11
/note=" tryptic'
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  carbon partitioning; plants.
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                                                                                                                                                                                                                                95; Conservative
                                                                                                                                                                                                             Similarity
                                                                                                                 993 AA;
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                                                                                                                      Sequence
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Maize sucrose phosphate synthase.
         11-MAY-1998 (first entry)
         NAME OF THE PROPERTY OF THE PR
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PQFEESM-----PVGPIYKKYNLSPNKKVLLIMAGAHGVLKNVKELCENLVKDDQVQVVV 235
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       278 -----ITKPGGITLIEATAIGVPVILYKPVPGQEKENANFFEDRGAAIVVNRHEE-- 327
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         The sequence, which is that of sucrose phosphate synthase (SPS), was deduced from a cDNA sequence obtd. from three clones isolated from a cDNA library prepd. From RNA isolated from corn leaves. The Liyptic peptides (see features) were used to design degenerative by PCR of a probe for the SPS gene. The gene can be used to prepare in sucrose regulation and carbon partitioning between starch and sucrose in photosynthesising plants. (Plants transformed with the DNA have an increased flow of sucrose to growing tissues and give increased yields). The recombinant SPS can be used to raise monoclonal antibodies which can then be used to purify the protein by
                                                                                                                                                                                                                                                                                                                                                                                                                              Sucrose phosphate synthase (SPS) from corn - its prepn., DNA encoding it, and hybridomas and monoclonal antibodies specific for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 1068;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Bruneau JM, Voelker TA, Gervais M;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                56; Mismatches 87; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    5.7%; Score 112.5; DB 13; 20.9%; Pred. No. 0.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             236 VCGKNTALKESLSALEAENGDKL-KVLGYVERID------
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636 iadallklvadknlwqecrrnglrnihl 663
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  885..891
/label= 12N
/note=" tryptic"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Claim 5; Fig 7; 40pp; English.
                                                                                                                                                                                 90EP-0402084
                                                                                                                                                                                                                         90EP-0402084
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       affinity chromatography.
                                                                                                                                                                                                                                                                                                                   Lando D,
                                                                                                                                                                                                                                                                      (ROUS ) ROUSSEL UCLAF
                                                                                                                                                                                                                                                                                                                                                           WPI; 1992-025895/04.
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                                                                                                                                                                                                                                                                                                                                                                                     N-PSDB; AAQ20664.
                                                                                                                                                                                                                                                                                                                   Van Assche C,
                                                                                                                                                                                                                       20-JUL-1990;
                                                                                                                                    22-JAN-1992
                                                                                       EP466995-A.
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This protein comprises maize sucrose phosphate synthase (SPS), an enzyme that catalyses the formation of sucrose phosphate from furctose 6-phosphate and UDP-glucose in photosynthetically active plant cells. It is considered to be a rate-limiting enzyme in the plant cells. It is considered to be a rate-limiting enzyme in the pathway providing sucrose to growing tissue. The SPS amino acid contains as deduced from CDNA clones (see AAT95847) derived from CDNA. The complete protein is believed to be a dimeric or tetrameric protein having a basic subunit of 110-130 kDa. Peptides to design primers (see AAM98270) isolated from SPS were used to design primers (see AAT95848-49) utilised in the isolation of SPS cDNA. Transgenic plants that express SPS can be used to measure the effects on crop yield of an increased rate of sucrose translocation to growing tissues.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DNA encoding sucrose phosphate synthase - useful for producing
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                                                                                  Location/Qualifiers
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                                        Lea mays L. cv. Pioneer 3184.
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N-PSDB; AAT95847.
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                            GRVIPTFNVM---TDFCLHKIWVHENVDKYYVATDYVKEKLLEI-GTHPSNVKITGIPIR 180
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Modifying sweetness of plant parts by introducing transgene that encodes sucrose phosphate synthase - also altering ratio of soluble solids in sink tissue, especially for increasing sugar content in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          The amino acid sequence (AAW09869) of maize hybrid 3184 sucrose phosphate synthase (SPS) was deduced from cDNA clones (see also AR766229) isolated from a leaf cDNA library. SPS is considered a rate-limiting enzyme in the pathway providing sucrose to growing tissue. Methods are provided for modifying the sweetness of plant sink tissue (partic, tomato fruit) in which SPS activity and/or invertase activity in plant tissues is manipulated. Carbohydrate partitioning can be modified in plant tissues and/or parts, which in turn can be used to alter plant growth, soluble solid content and/or sweetness, and/or to alter the sensitivity of plant growth to temperature and/or to levels of carbon dioxide and oxygen.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                sweetness; transgenic plant; tomato;
corn.
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Best Local Similarity 20.9%; Pred. No. 0.1;
Matches 56; Conservative 56; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  174 ITGIPIRPQFEE-SMPVGPIYKKYNLSPNKKVLLIMAGAHGVLKNVKELCENL-VKDDQV 231
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       |:: : | | :|| :| :::: :|| ::: | |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |::::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |::| |:::| |::| |:::| |:::| |:::| |:::| |:::|
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  PIRPQFEESMPVGPIYKKY-----NLSPNKKVLLIMAGAHGVLKNVKELCEN-LVKDDOV
                               QVVVVCGKNTALKESLSALEAENGDKLK------VLGYVERIDELFRITDCMITKPGGIT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       173 PTGIPI-PNLESIDQPKWKVRNDLGLDPQRKVLIIAGGGIG-LTNYAQVIRALECLPEPI
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 374;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Ouery Match 18.7%; Score 368; DB 2; Length 37 Best Local Similarity 27.0%; Pred. No. 6.1e-16; Matches 103; Conservative 84; Mismatches 159; Indels
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Takani H., Nakasone K., Takaki Y.;
Submitted (MAR-2000) to the EMBL/GenBank/DDBJ databases.
EMBL; AP001513; BABD5676.1;
SEQUENCE 374 AA; 42361 MW; DA96A0EA33C5AC65 CRC64;
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Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Bacillus/Clostridium group;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            374 AA.
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NCBI_TaxID-86665;
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                                                                                                                                                                                                                                                                                               346 KKNIKDLHLANSSEVILEDIL 366
                                                                                                                                                                                                                                                                                                                                   346 ISTMEQDKIKYATQTICRDLL 366
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Best Local Similarity
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178
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RESULT

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64 I------GKQFYRLFYYGVDKIYNKRKFNIYFKM----GNKRLGELVDEHQPDIIIN 110
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           169 PSNVKITGIPIRPQFEESMPV-----GPIYKKYNLSPNKKVLLIMAGAHGVLKNVKELC 222
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           29 RALFMSVSLGAGHDQA----QQAVKQAFAERGVELLGAEHDSV----EYLSTFERSFT 78
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         R.D.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            223 ENLVK-DDQVQVVVVCGKNTALKESLSALEAENGDKLKVLGYVERIDELFRITDCMITKP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      256 TELGNLGRAVOVLVPASRQGEGTETI-----GGATVHHLGFRRDLPRLLAASDLVVGKA
                                                                                                                                                                              Deinococcus radiodurans.
Bacteria; Thermus/Deinococcus group; Deinococcus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      "Genome sequence of the radioresistant bacterium Deinococcus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 411;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              164; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   D825DE52B8801437 CRC64;
                                              01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-MAY-2001 (TrEMBLrel. 16, Last annotation update)
CELL WALL SYNTHESIS PROTEIN, PUTATIVE.
DR1076.
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01-MAY-2000 (TrEWBLrel. 13, Created)
01-MAY-2000 (TrEWBLrel. 13, Last sequence update)
01-MAR-2001 (TrEWBLrel. 16, Last annotation update)
MGDG SYNTHASE A PRECURSOR (EC 2.4.1.46).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Science 286:1571-1577(1999).
EMBL: AE001958; AFF10649-1; -.
TIGR: DR1076; -.
SEQUENCE 411 hr.
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Spinacia oleracea (Spinach)
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PRELIMINARY;
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Best Local Similarity
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Buell C.R., Ketchum K.A., Lee J.J., Ronning C.M., Koo H., Moffat K.S., Cronin L.A., Shen M., VanAken S.E., Umayam L., Tallon L.J., Gill J.E., Adams M.D., Carrera A.J., Creasy T.H., Goodman H.M., Somerville C.R., Copenhaver G.P., Preuss D., Nierman W.C., White O., Elsen J.A., Salzberg S.L., Fraser C.M., Venter J.C.; "Sequence and analysis of chromosome II of Arabidopsis thallana."; Mature 402:761-768(1999).

EMBL, AC007187, AAD28678.1; -...
                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                72 KTVLILMSDTGGGHRASAEAI-RDAFKIEFGDDYRIIIKDVWKEYTGWPLNDMERQYKFM 130
                                                                                                                                                                                                                                                                                                                                                                                                    60 KSFSIGKQFYRLFYYGVD-KIYNKRKFNIYFKMGNKRLGELVDEHQPDIIINTFPM---- 114
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          307 KESNPIGQLIVICGRNKVLASTLASHEWR--IPVKVRGFETQMEKWMGACDCIITKAGPG 364
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             365 TIAEALICGLPIILNDYIPGQEKGNVPYVVDNGAGVFTRSPKETAKIVADWFSNNKEELK 424
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                                                                                                                                                                                                                                                                                                                              5 KRVLILTANYGNGHVQVAKTLYEQCVRLGF---QHVTVSNLYQESN--PIVSEVTQYLYL 59
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Eukaryota, Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta;
Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids II;
Brassicales; Brassicaceae; Arabidopsis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Η.,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                         115 -IVVPEYRRTGRVIPTFNVMTDF-CLHKIWVHENVDKYYVATDYVKEKLLEIGTHPSNV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             173 KITGIPIRPOFEES-MPVGPIYKKYNLSPNKKVLLIMAGAHG---VLKNVKELCENLVKD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           285 TLTEATAIGVPVILYKPVPGQEKENANFFEDRGAAIVVNRHEEILESVTSLLA-DEDTLH
                                                                                                                                                                                                                                                                                                                                                                                                                          229 DQV----QVVVVCGKNTALKESLSALEAENGDKLKVLGYVERIDELFRITDCMITKPGGI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.

Awai.K., Marechal E., Block M.A., Takamiya K., Joyard J., Ohta I.

"The Multigenic Family of MGDG synthases.";

Submitted (AUG-2000) to the EMBL/GenBank/DDBJ databases.

EMBL, AB04/398; BAB12041.1;

SEQUENCE 465 AA; 52990 MW; 05E0157012E50A14 CRC64;
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                                                                                                                                                                                                                                                          Length 464;
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                                                                                                                                                                                 PF00534; Glycos_transf_1; 1.
ice 464 AA; 52859 MW; FEC2B424CFBBA136 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                      16.1%; Score 317; DB 10; 25.6%; Pred. No. 1.5e-12; ive 90; Mismatches 171;
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25.6%; Pred. No. 1.5e-12;
tive 90; Mismatches 171;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                344 RMKKNIKDLHLANSSEVILEDILKESEMMTAKOK 377
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Arabidopsis thaliana (Mouse-ear cress).
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                                                                                                                                                                                                                                                      Query Match
Best Local Similarity 25.69
Matches 101; Conservative
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es 101; Conserv
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Best Local Si
Matches 101;
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REQUENCE FROM N.A.
MEGG-10518794;
Miege C., Marechal E., Shimojima M., Awai K., Block M.A., Ohta H.,
Takamiya K.I., Douce R., Joyard J.;
"Biochemical and topological properties of type A MGDG synthase, a
spinach chloroplast envelope enzyme catalyzing the synthesis of both
prokaryotic and eukaryotic MGDG.";
Eur. J. Biochem. 265:990-1001(1999).
EMBL; AJ249607; CAB550181; -.
Transit peptide; Transferase; Glycosyltransferase.
"BABC, AJ249607; CAB50181; -.
"MGDG SYNTHASE A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 243 MQHVPLRILRGRGLLEKIVFTTVVTDLSTCHPTWFHKLVTRCYCPSNEVAKRATKAGLQP 302
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           478
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           115 IVVPEYRRTGR----VIPTFNVMTDF-CLHKIWVHENVDKYYVATDYVKEKLLEIGTHP 169
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 282 GGITLTEATAIGVPVILYKPVPGQEKENANFFEDRGAAIVVNRHEEILESVTSLLADEDT 341
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          56 YLYLKSFSIGKQFYRLFYYGVD-KIYNKRKFNIYFKMGNKRLGELVDEHQPDIIINTFPM 114
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            227 KDDQV----QVVVVCGKNTALKESLSALEAENGDKLKVLGYVERIDELFRITDCMITKP 281
                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
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STRAIN-CV. COLUMBIA.
MEDLINE-20083487; Pubmed-10617197;
Lin X., Kaul S., Rounsley S.D., Shea T.P., Benito M.-I., Town C.D.,
Fujli C.Y., Mason T.M., Bowman C.L., Barnstead M.E., Feldblyum T.V.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                       5 KRVLILTANYGNGHVQVAKTLYEQCVRLGFQ-----HVTVSNLYQESN--PIVSEVTQ 55
Eukaryota; Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta;
Magnoliophyta; eudicotyledons; core eudicots; Caryophyllidae;
Caryophyllales; Chenopodiaceae; Spinacia.
NCBI_TaxID=3562;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Eukaryoja; Viridiplantas; Embryophyta; Tracheophyta; Spermatophyta;
Magnollophyta; eudicotyledons; core eudicots; Rosidae; eurosids II;
Brassicales; Brassicaceae; Arabidopsis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      170 SNVKITGIPIRPQFEESM-PVGPIYKKYNLSPNKKVLLIMAGAHGV--LKNVKELCENLV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      48;
                                                                                                                                                                                                                                                                                                                                                                               Length 522;
                                                                                                                                                                                                                                                                                                                                                                                                                     Indels
                                                                                                                                                                                                                                                                                                         MGDG SYNTHASE A.
02E2B929732551A7 CRC64;
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01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-CT-2000 (TrEMBLrel. 15, Last annotation update)
PUTATIVE MONOGALACTOSYLDIACYLGLYCEROL SYNTHASE.
                                                                                                                                                                                                                                                                                                                                                                                                                   80; Mismatches 162;
                                                                                                                                                                                                                                                                                                                                                                               Score 326; DB 10;
Pred. No. 4.6e-13;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     464 AA.
                                                                                                                                                                                                                                                                                                                                                                               16.5%; Score 326; 25.3%; Pred. No. 4
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                342 LHRMKKNIKDLHLANSSEVILEDILKES 369
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                   98; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRELIMINARY;
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Azevedo V., Bertero M.G., Bessieres P., Bolotin A., Borchert S.,
Borriss R., Boursier L., Brans A., Braun M., Brignell S.C., Bron S.,
Bornist S., Bruschi C.V., Caldwell B., Capuano V., Carter N.M.,
Choi S.K., Codani J.J., Connerton I.F., Cummings N.J., Daniel R.A.,
Brian K.D., Errington J., Fabret C., Ferrari E., Foulger D. P.T.,
Brian K.D., Errington J., Fabret C., Ferrari E., Foulger D.
Fritz C., Fujita M., Fujita Y., Fuma S., Galizzi A., Galleron N.,
Guiseppi G., Guy B.J., Haga K., Haicch J., Harwood C.R., Henaut A.,
Hilbert H., Holsappel S., Hosono S., Hullo M.F., Itaya M., Jones L.,
Joris B., Karamata D., Kasahara Y., Klaerr-Blanchard M., Klein C.,
Kobayashi Y., Koetter P., Koningstein G., Krogh S., Kumano M.,
Kurita K., Lapidus A., Lardhols S., Lauber J., Lazarevic V.,
Lee S.M., Levine A., Liu H., Masuda S., Mauel C., Medigue C.,
Moone D., O'Reilly M., Ogawa K., Wostlik S., Prescott A.M.,
Parro V., Pohl T.M., Portetelle D., Porwollik S., Prescott A.M.,
Presecan E., Pujic P., Purnelle B., Rapoport G., Rey M., Reynolds S.,
R Rieger M., Rivolta C., Rocha E., Roche B., Rose M., Sadaie Y.,
Sato T., Scanlan E., Schleich S., Schroeter R., Stin B.S., Soldo B.,
Sekiguchi J., Sekowska A., Seror S.J., Serror P., Shin B.S., Soldo B.,
                                                                           132 VK-HVG--LWSVAFHGTSPRWIHKSYLSALAAYYAKEIEAGLMEYKPDIIISVHPLMQHI 188
                                                                                                                                                                                                                                                                                                                   36 TIAEALICGLPIILNDYIPGQEKGNVPYVVDNGAGVFTRSPKETAKIVADWFSNNKEELK 425
                          73 KTVLILMSDTGGGHRASAEAI-RDAFKIEFGDDYRIIIKDVWKEYTGWPLNDMERQYKFM 131
                                                                                                                  115 -IVVPEYRRTGRVIPTFNVMTDF-CLHKIWVHENVDKYYVATDYVKEKLLEIGTHPSNV 172
                                                                                                                                                                                                                                                                                             TLTEATAIGVPVILYKPVPGQEKENANFFEDRGAAIVVNRHEEILESVTSLLA-DEDTLH 343
5 KRVLILTANYGNGHVQVAKTLYEQCVRLGF---QHVTVSNLYQESN--PIVSEVTQYLYL 59
                                                                                                                                      348 RVFGLPVRPSFPRTILNKNELRKELEIDINLPAVILMGGGEGMGPVQKTALALGDSLYNS
                                                                                                                                                                                                                                       DQV----QVVVVVCGKNTALKESLSALEAENGDKLKVLGYVERIDELFRITDCMITKPGGI
                                                                                                                                                                                                                                                     60 KSFSIGKQFYRLFYYGVD-KIYNKRKFNIYFKMGNKRLGELVDEHQPDIIINTFPM----
                                                                                                                                                                              KITGIPIRPQFEES-MPVGPIYKKYNLSPNKKVLLIMAGAHG---VLKNVKELCENLVKD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STRAIN=168;
Devine K.M.;
Submitted (NOV-1997) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Bacteria, Firmicutes, Bacillus/Clostridium group, Bacillus/Staphylococcus group; Bacillus.
                                                                                                                                                                                                                                                                                                                                                                       344 RMKKNIKDLHLANSSEVILEDILKESEMMTAKQK 377
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Created)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRELIMINARY;
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Bacteria; Firmicutes;
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Sorokin A., Tacconi E., Takagi T., Takahashi H., Takemaru K., Takuchi M., Tanakoshi A., Tanaka T., Terpstra P., Tognoni A., Tosato V., Uchiyama S., Vandenbol M., Vannier F., Vassarotti A., Viari A., Wambutt R., Wedler E., Wedler H., Weitzenegger T., Winters P., Wipat A., Yamamoto H., Yamane K., Yasumoto K., Yata K., Yoshida K., Yoshikawa H.F., Zumstein E., Yoshikawa H.F., Zumstein E., Yoshikawa H., Danchin A.; The complete genome sequence of the gram-positive bacterium Bacillus
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         115 IVV----PEYRRRIGRVIPTFNVMTDFCLHKIWVHENVDKYYVATDYVKEKLLEIGTHPS 170
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       64 IGKQFYRLFYYGVDKI-----YNKRKFNIYFKMGNKRLGELVDEHQPDIIINT--FPM 114
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Spermatophyta;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          2 KNILIFPFLSISTGHHHVADALQAELESQGLAAEKI-DIFSHSYRRLEKLSSVAYLKWI-
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NLVKDDQVQVVVVCGKNTALKESLSALEAENGDKLKVLGYVERIDELFRITDCMITKPGG
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Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids
Cucurbitales; Cucurbitaceae; Cucumis.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           15.7%; Score 309; DB 2; Length 373
24.6%; Pred. No. 3.5e-12;
tive 89; Mismatches 158; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Kunst F., Ogasawara N., Yoshikawa H., Danchin A.;
Submitted (NOV-1997) to the EMBL/GenBank/DDBJ databases.
EMBL; 240102571; CA405612.1; -
EMBL; 299111; CAB13208.1; -
EMBL; 299110; CAB13192.1; -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       62FFCF2BDC598CDC CRC64;
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MEDILNE=9714442; PubMed=8990209;
Shimojima M., Ohta H., Iwamatsu A., Masuda T., Shioi
Takaniya K.-I.;
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01-JUN-1998 (TrEMBLrel. 06, Created)
01-JUN-1998 (TREMBLrel. 06, Last sequence update)
01-MAR-2001 (TrEMBLrel. 16, Last annotation update)
MONOGALACTOSYLDIACYLGIYCEROL SYNTHASE PRECURSOR (EC
(1,2-DIACYLGIYCEROL 3-BETA-GALACTOSYLTRANSFERASE).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             340 DTLHRMKKNIKDLHLANSSEVILEDILKESEMMTAKQKAKVL 381
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       373 AA; 43480 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Cucumis sativus (Cucumber).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Ouery Match
Best Local Similarity 24.69
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Nature 390:249-256(1997).
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57839 MW; D33C37FD53E90218 CRC64;

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      530
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      SEQUENCE
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255 ILRSKGLLNKIVFT-TVVTDLSTCHPTWFHKLVTRCYCPSTEVAKRALTAGLQPSKLKVF 313
                                                                                                                                                                                                                                                                                                                                                                           62 FSIGKQFYRLFYYGVDKIYNKRKFNIYFKMGNKRLGELVDEHQPDIIINTFPM----IV 116
                                                                                                                                                                                                                                                                                             117 VPEYRRRTGRVIPTFNVMTDF-CLHKIWVHENVDKYYVATDYVKEKLLEIGTHPSNVKIT 175
                                                                                                                                                                                                                                                                                                                                                                                                                                          286 LTEATAIGVPVILYKPVPGQEKENANFFEDRGAAIVVNRHEEILESVTSLLADE-DTLHR 344
                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Glycine max (Soybean).

Bukaryota, Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta;

Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids I;

Fabales; Fabaceae; Papilionoideae; Glycine.
                                                                                                                                                             MONOGALACTOSYLDIACYLGLYCEROL SYNTHASE: 74FE586082EC48BA CRC64;
                                                                                                                                                                                                                                           5 KRVLILTANYGNGH---VQVAKTLYEQCVRLGFQHVTVSNLYQESNPIVSEVTQYLYLKS
                                                                                                                                                                                                                                                                                                                                                              176 GIPIRPQFEESMPVGP---IYKKYNLSPNKKVLLIMAGAHG---VLKNVKELCENLVKDD
                                                                                                                                                                                                                                                                                                                                                                                                    230 Q----VQVVVVCGKNTALKESLSALEAENGDKLKVLGYVERIDELFRITDCMITKPGGIT
                                                                                                                                                                                                                                                                                                                                                                                                                EMBL; U62622; AAC49624.1; ...
Mendel; 12656; Cucsa;1856;12656.
Transferase; Glycosyltransferase; Transit peptide; Chloroplast.
                                                                                                                                                                                                                         33;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Awai K., Takamiya K., Ohta H.;
ToDNa cloning of MGDG synthase from tobacco and soybean.";
Submitted (AUG-2000) to the EMBL/GenBank/DDBJ databases.
EMBL; AB047475; BAB11979.1;
                                                                                                                                                                                                      Length
                                                                                                                                                                                                   15.4%; Score 303.5; DB 10; Length 25.7%; Pred. No. 1.3e-11; ive 77; Mismatches 179; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      530 AA.
                                                                                                                                                     CHLOROPLAST
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    490 MSQNA--LRLARPDAVFKIVHDLHELVKQ 516
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Created)
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                                                                                                                                                                      57862 MW;
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                                                                                                                                                                                                                       Matches 100; Conservative
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01-MAR-2001 (TrEMBLrel.
01-MAR-2001 (TrEMBLrel.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MGDG SYNTHASE TYPE A.
                                                                                                                                                                      525 AA;
                                                                                                                                                                                                               Best Local Similarity
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                                                                                                                                                                                                                                                            316 FGLPVRPSFVK--PVQPKDELRRELGMDEDLPAVLLMGGGEGMGPIEATARALGDSLY-D 372
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    229 DQV-----QVVVVCGKNTALKESLSALEAENGDKLKVLGYVERIDELFRITDCMITKPGG 283
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    284 ITLTEATAIGVPVILYKPVPGQEKENANFFEDRGAAIVVNRHEEILESVTSLLADED-TL 342
                                                                                                                                                                 139 KKVLILMSDTGGGHRASAEAIKAAFYQEFGDDYQ-VFVTDLWADHTPWPFNQLPRSY--S 195
                                                                                                                                                                                                                         62 FSIGK-OFYRLFYYG-VDKIYNKRKFNIYFKMGNKRLGELVDEHQPDIIINTFPMI--VV 117
                                                                                                                                                                                                                                                                                                                                     118 PEYRRRIG -- RVIPTFNVMTDF-CLHKIWVHENVDKYYVATDYVKEKLLEIGTHPSNVKI 174
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   431 GTIAEAQIRGLPIILNDYIAGQEAGNVPYVVENGCGKFSKSPKDIAKIVAEWFGPKAYEL 490
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Jarvis P., Doermann P., Peto C.A., Lutes J., Benning C., Chory J.;
"Galactolipid-Deficiency and Abnormal Chloroplast Development in the
Arabidopsis AndD Synthase I Mutant.";
Proc. Natl. Acad. Sci. U.S.A. 0:0-0(2000).
EMBL; AF241797; AAF65066.1; -
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Eukaryota; Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta;
Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids II;
Brassicales; Brassicaceae; Arabidopsis.
NCBI_TAXID=3702;
                                                                                                                                                                                                                                                                                                                                                                                             256 LRILRSKGLLKKIVFTTVITDLSTCHPTWFHKLVTRCYCPTTDVAQRALKAGLQQSQIKI
                                                                                                                                                                                                                                                                                                                                                                                                                                                     175 (TGIPIRPOFEESMPVGP---IYKKYNLSPNKKVLLIMAGAHG---VLKNVKELCENLVKD
                                                                                                            5 KRVLILTANYGNGH----VQVAKTLYEQCVRLGFQHVTVSNLYQESNPIVSEVTQYLYLKS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    5 KRVLILTANYGNGHVQVAKTLYEQCVRLGFQ-----HVTVSNLYQESN--PIVSEVTQ
                                                       34;
     Length 530;
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01-0cT-2000 (TrEMBLrel. 15, Last sequence update)
01-0cT-2000 (TrEMBLrel. 15, Last annotation update)
MONOGALACTOSYLDIACYLGIXCEROL SYMPHASE.
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; Score 302; DB 10;
; Pred. No. 1.6e-11;
79; Mismatches 168;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             343 HRMKKNIKDLHLANSSEV--ILEDI 365
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  491 OOMSONA -- LRLARPDAVFKIVHDL 513
15.3%;
llarity 27.0%;
Conservative 7
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Best Local Similarity 24.8
Matches 101; Conservative
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197 YNFLVKHG---TLWKMTYYGTSPRIVHQSNFAATSTFIAREIAQGLMKYQPDIIISVHPL 253
                                                                                              I -- VVPEYRRRIG -- RVIPTFNVMTDF - CLHKIWVHENVDKYYVATDYVKEKLLEIGTHP 169
                                                                              SNVKITGIPIRPQFEESMPVGP---IYKKYNLSPNKKVLLIMAGAHGV--LKNVKELCEN 224
                                                                                                                                                                                  280 KPGGITLIEATAIGVPVILYKPVPGQEKENANFFEDRGAAIVVNRHEEILESVTSLLAD- 338
                                                                                                                                                                                                                                                                                                                                                                     01-NOV-1998 (TrEMBLrel. 08, Last sequence update)
01-MAR-2001 (TrEMBLrel. 16, Last annotation update)
MONOGALACTOSYLDIACYLGIXCEROL SYNTHASE - LIKE PROTEIN
(MONOGALACTOSYLDIACYLGIXCEROL SYNTHASE-LIKE PROTEIN) (MGDG SYNTHASE
                                                                                                                                                                                                                                                                                                                                                                                                                                                  Arabidopsis thaliana (Mouse-ear cress).
Bukaryota, Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta;
Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids II;
Brassicales; Brassicaceae; Arabidopsis.
                                          Terryn N., Ardiles W., Buysshaert C., Dasseville R., De Clerck R., Ge Keyser A., Meyt P., Rouze P., Van Den Daele H., Villaroel R., Gielen J., Van Montagu M., Mewes H.W., Lencke K., Mayer K.F.X.; Submitted (MAR-2000) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                  LVKDDQV-----QVVVVCGKNTALKESLSALEAENGDKLKVLGYVERIDELFRITDCMIT
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M.;
                                                                                                                                                                                                                                     339 ----EDTLHRMKKNIKDLHLANSSEVILEDILKESEMMTAKQKAKVLS 382
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Rieger M., Mueller-Auer S., Zipp M., Schaefer M., Mewes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Lemcke K., Mayer K.F.X.; Submitted (MAR-2000) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EU Arabidopsis sequencing project;
Submitted (MAR-2000) to the EMBL/GenBank/DDBJ databases
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Wal K., Marechal E., Block M.A., Takamiya K., Joyard ...
The Multigenic Family of MGDG synthases.";
EMBL, AL012000) to the EMBL/GenBank/DDBJ databases
EMBL, AL031004, CAA19745.1;
EMBL, AL041579; CAB79896.1;
EMBL, AB047399; BAB12042.1;
EMBL, AB047399; BAB12042.1;
SEQUENCE 533 AA; 58537 MW; E581E67317CB9CC8 CRC64;
                                                                                                                                                                                                                                                     486 FGPASKELEIMSQNA--LRLA-KPEAVFKIVHDMHELVRKKNSLPQLS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Rieger M., Mueller-Auer S., Zipp M., Schaefer
Mewes H.W., Mayer K.F.X., Schueller C., Bevan
Submitted (JUN-1998) to the EMBL/denBank/DDBJ
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                                                                                                                                                                                                                                                                                                                                                           Created)
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Lemcke K.
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DB 10; Length 533;

Score 301.5; DB 1 Pred. No. 1.7e-11;

15.3%;

Query Match Best Local Similarity

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                                                                          KKVLILMSDIGGGHRASA----EAIRAAFNQEFGDEYQVFITDLWIDHIPWPFNQLPRS 196
                                                                                                                                                                                                            115 I--VVPEYRRTG--RVIPTFNVMTDF-CLHKIWVHENVDKYYVATDYVKEKLLEIGTHP 169
                                                                                                                                                        224
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                                          KRVLILTANYGNGHVQVAKTLYEQCVRLGFQ-----HVTVSNLYQESN--PIVSEVTQ 55
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Magnoliophyta; eudicotyledons; core eudicots; Asteridae; euasterids
Solanales; Solanaceae; Nicotiana.
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                                                                                                                                                                                                                                                                                                                       YLYLKSFSIGKQFYRLFYGVD-KIYNKRKFNIYFKMGNKRLGELVDEHQPDIIINTFPM
                                                                                                                                                                                                                                           : | : | : | : | : | 254 MQHVPLRVLRSKGLLKKIVFTTVITDLSTCHPTWFHKLVTRCYCPSTEVAKRAQKAGLET
                                                                                                                                                                                                                                                                                               SNVKITGIPIRPQFEESMPVGP---IYKKYNLSPNKKVLLIMAGAHGV--LKNVKELCEN
                                                                                                                                                                                                                                                                                                                                                                               225 LVKDDQV-----QVVVVCGKNTALKESLSALEAENGDKLKVLGYVERIDELFRITDCMIT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    145 KKVLILMSDIGGGHRASA-----EAIRSAFNEEFGDKYQVFITDLWTEHTPWPFNQLPRS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  200 YNFLVKHGSLWRMTYYATAPRLVHQTNFAATSTFIAREVAKGLMKYQPDIIISVHPLMQH
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       YLKSFSIGKQFYRLFYYGVDKIYNKRKFNIYFKMGNKRLGELVDEHQPDIIINTFPMI--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          116 VVPEYRRRTG----RVIPTFNVMTDF-CLHKIWVHENVDKYYVATDYVKEKLLEIGTHPSN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         172 VKITGIPIRPQFEESMPVGP---IYKKYNLSPNKKVLLIMAGAHG---VLKNVKELCENL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              42;
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Awai K., Takamiya K., Ohta H.;
CDNA cloning of MGDG synthase from tobacco and soybean.";
Submitted (AUG-2000) to the EMBL/GenBank/DDBJ databases.
EMBL; AB04/476; BAB11980.1; -.
SEQUENCE 535 AA; 59589 MW; B1B2067E86EDE477 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   486 FGPASKELEIMSQNA--LRLA-KPEAVFKIVHDMHELVRKKNSLPQLS 530
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ----EDTLHRMKKNIKDLHLANSSEVILEDILKESEMMTAKQKAKVLS 382
    Indels
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Last annotation update)
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.5e-11;
es 169;
    86; Mismatches 172;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Created)
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16,
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Best Local Similarity 26.2
Matches 102; Conservative
101; Conservative
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01-MAR-2001 (TrEMBLrel.
01-MAR-2001 (TrEMBLrel.
MGDG SYNTHASE TYPE A.
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  Matches
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us-09-668-788-2.rspt

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14;
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STRAIN-CV. COLUMBIA.
Awai K., Shimojima M., Masuda T., Takamiya K.I., Ohta H.;
"cDNA cloning of an Arabidopsis monogalactosyldiacylglycerol synthase revealed that the enzyme belongs to an uridine diphosphate-utilizing glycosyltransferase superfamily.";
Submitted (JUL-1998) to the EMBL/GenBank/DDBJ databases.
EMBL; AJO00311; CAA04005.1;
Mendel; 33300; Arath;1856;33300.
InterPro; IPR000566;
PROSIȚE; PS00213; LIPOCALIN; UNKNOWN_I.
                    QHIPLWYLKWQELQKRVL-FYTVITDLNTCHPTWFHPGVNRCYCPSQEVAKRALFDGLDE 240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         241 SQVRVFGLPVRPSFARAVLVKDDLRKELEMDQDLRAVLLMGGGEGMGPVKETARALEEFL 300
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         | |: |: :| : :| | GPGTIAESLIRSLPIILNDYIPGQEKGNVPYVVENGAGVFTRSPKETARIVGEWFSTKTD 418
226 VKDDQV-----QVVVVCGKNTALKESLSALEAENGDKLKVLGYVERIDELFRITDCMIT 279
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SFSIGKQFYRLFYYG-----VDKIYNKRKFNIYFKMGNKRLGELVDEHQPDIIINTFPM- 114
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         129 KH---VOLWKVAFHSTSPKWIHSCYLAAIAAYYAKEVEAGL----MEYKPEIIISVHPLM 181
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ----IVVPEYRRRTGRVIPŢFNVMTDF-CLHKIWVHENVDKYYVATDYVKEKLLEIGTHP 169
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    KRVLILTANYGNGHVQVAKTLYEQC-VRLGFQH-VTVSNLYQESN--PIVSEVTQYLYLK 60
                                                                                                                                                                                                                                                                                                                                                                                            Arabidopsis thaliana (Mouse-ear cress).
Eukaryota: Viridiplantae: Embryophyta: Tracheophyta; Spermatophyta;
Bagnoliophyta: eudicotyledons; core eudicots; Rosidae; eurosids II;
Brassicales; Brassicaceae; Arabidopsis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SNVKITGIPIRPQFEESMPV-GPIYKKYNLSPNKKVLLIMAGAHGV--LKNVKELCENLV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            227 KDDQ-----VQVVVVCGKNTALKESLSALEAENGDKLKVLGYVERIDELFRITDCMITKP
                                                                     280 KPGGITLTEATAIGVPVILYKPVPGQEKENANFFEDRGAAIVVNRHEEILESVTSLLAD-
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.ive 86; Mismatches 172; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Glycosyltransferase.
88 AA; 52726 MW; 58F56C3C1C383C24 CRC64;
                                                                                                                                                                                                                                                                                                                        01-NOV-1998 (TrEMBLrel. 08, Last sequence update)
01-MAR-2001 (TrEMBLrel. 16, Last annotation update)
MONGGALACTOSYLDIACYLGIXCEROL SYNTHASE (EC 2.4.1.46)
MGD.
                                                                                                                                                                                                                                                                      468 AA.
                                                                                                                                                                  :| | | :| | 1| | 1| | 4| 3| QDELRIMSQNA--LRLARPDAVFKIVHDM 519
                                                                                                                                          339 EDTLHRMKKNIKDLHLANSSEV--ILEDI 365
                                                                                                                                                                                                                                                                                                            Created)
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Best Local Similarity 25.1
Matches 98; Conservative
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082730
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65 GKOFYRLFYYGVDKIY---NKRKFNIYFKMGNKR-----LGELVDEHQPDIIINTFPMI 115
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GTHPSNVKITGIPIRPOFEESMPVGPIYKKY---NLSPNKKVLLIMAGAHGVLKNVKELC 222
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        46; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RRLLVISASMGAGHDTVAAELVRRARERGDTAQTV-------DVLALLPYGL 59
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STRAIN-A3(2));

MEDLINE-97000351; PubMed-8843436;

Redenbach M., Kleser H.M., Denapaite D., Eichner A., Cullum J.,

Kinashi H., Hopwood D.A.;

"A set of ordered cosmids and a detailed genetic and physical map:

the 8 Mb Streptomyces coelicolor A3(2) chromosome.";

Mol. Microbiol. 21:77-96(1996).

EMBL; AL445503; CAC13078.1; --

SEQUENCE 384 AA: 40689 MW; E64E01E05B1DDE40 CRC64;
                                                                                                                                                                                                                           Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;
Actinomycetales; Streptomycineae; Streptomycetaceae; Streptomyces.
NCBL TaxID=1902;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         236 VRLLVDHGYLPVVLCGDNQRLRRTLSGTPG----VLALGWVTDMPGLLHAARALIDNAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   5 KRVLILTANYGNGHVQVAKTLYEQCVRLGFQHVTVSNLYQESNPIVSEVTQYLYLKSFSI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    177 GNTGTPAETCGPVVAPEFSAGRVPGAAQWRETFDRLGPGRPAVVLSAGAWGVGSHL-DAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ENLVKDDQVQVVVVCGKNTALKESLSALEAENGDKLKVLGYVERIDELFRITDCMITKPG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  283 GITLTEATAIGVPVILYKPVPGQEKENANFFEDRGAAIVVNRHEEILESVTSLLA 337
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  11.0%; Score 216; DB 2; Length 384; ilarity 22.8%; Pred. No. 3e-06; Conservative 61; Mismatches 167; Indels 4
                                                                                                                                                                                                                                                                                                                                                                                        STRAIN=A3(2);
Cerdeno A.M., Parkhill J., Barrell B.G., Rajandream M.A.;
Submitted (>CT-2000) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                         STRAIN=A3(2);
Saunders D.C., Harris D.;
Submitted (OCT-2000) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                              Last sequence update)
Last annotation update)
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01-MÅR-2001 (TrEMBLrel. 16,
01-MÅR-2001 (TrEMBLrel. 16,
PUTATIVE SECRETED PROTEIN.
                                                                                                 PRELIMINARY;
                                                                                                                                                                                                               Streptomyces coelicolor.
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Best Local Similarity
Matches 81; Conserv
                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
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Q9K9T0;
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                                                                                               Q9EX00
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                                                               RESULT
Q9EX00
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341 TLHRMKKNIKDLHLANSSEVILEDILKESE 370

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                                                                                                                                                                                                                                                                                                                                                                                                                                                     123 QNSVPGLINKFLSRYVDRIAICFKEABAFFPKNKVVFTGNPRASEVMSGNREEGL---- 177
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              193 YKKYNLSPNKKVLLIMAGAHGVLKNVKELCENLVKDDQV---QVVVVCG--KNTALKESL 247
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 248 SAL-EAENGDKLKVLGYVERIDELFRITDCMITKPGGITLTEATAIGVPVILYKPVP--- 303
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    304 -GQEKENANFFEDRGAAIVVNRHE----EILESVTSLLADEDTLHRMKKNIKDLHLANSS 358
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  54; Gaps
01-OCT-2000 (TrEMBLrel. 15, Created)
01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
01-OCT-2000 (TrEMBLrel. 15, Last annotation update)
01-OCT-ACETYLGLUCOSAMINE-N-ACETYLAURAMYL-(PENTAPEPTIDE)PYROPHOS.
                                                                                                                                                                                                                                                                                              Query Match
9.0%; Score 178; DB 2; Length 363;
Best Local Similarity 23.1%; Pred. No. 0.00074;
Matches 72; Conservative 62; Mismatches 124; Indels
                                                                                                                                                            SERAIN-C-125 / JCM 9153;
STRAIN-C-125 / JCM 9153;
Takami H., Nakasone K., Takaki Y.;
Submitted (MAR-2000) to the EMBL/GenBank/DDBJ databases.
EMBL; AP001515; BAB06284.1; --
SEQUENCE 363 AA; 39715 MW; 3RJDD063E495EEIB CRC64;
                                                                         MUKG.

Bacillus halodurans.

Bacillus/Clostridium group;

Bacillus/Staphylococcus group;

NCBI_TaxID=86665;
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EKLHMLVKEVAK 363
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Search completed: June 29, 2001, 09:05:02 Job time: 319 sec

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GenCore version 4.5

Copyright (c) 1993 - 2000 Compugen Ltd.

OW protein - protein search, using sw model

Run on:

June 29, 2001, 08:56:42; Search time 24:11 Seconds (without alignments)

319:173 Million cell updates/sec

Title:

US-09-668-788-2

Perfect score:

1970

Sequence:

LMMTMKRVLILTANYGNGHVQ......EDILKESEMMTAKQKAKVLS 382

Scoring table:

Gapop 10.0, Gapext 0.5

Searched:

193259 seqs, 20144635 residues

Total number of hits satisfying chosen parameters:

Total number of hits satisfying chosen parameters:

Minimum DB seq length: 2000000000

Post-processing: Minimum Match 10%

Maximum Match 10%

Listing first 45 summaries
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

Issued\_patents\_AA:\*
1: /cgn2\_6/ptodatv2/iaa/5A\_COMB.pep:\*
2: /cgn2\_6/ptodatv2/iaa/5B\_COMB.pep:\*
3: /cgn2\_6/ptodata/2/iaa/6A\_COMB.pep:\*
4: /cgn2\_6/ptodata/2/iaa/6B\_COMB.pep:\*
5: /cgn2\_6/ptodatu2/iaa/PCTUS\_COMB.pep:\*
6: /cgn2\_6/ptodatu2/iaa/PCTUS\_COMB.pep:\*

Database

## SUMMARIES

	Description	Sequence 86, Appl	11,	7.7		7	12,	12,	12,	36,	2, 4	Sequence 10, Appl	7	4	Sequence 2, Appli	7,	4	7	4	Sequence 2, Appli	85,	9	ď,	7	Sequence 4, Appli	'n	7	7
SUMMARIES	ID	US-08-846-762-86	US-08-429-054A-11	US-08-718-777-7	US-09-051-341-7	PCT-US92-00282-7	US-07-977-434-12	US-08 458-819-12	PCT-0391-07035-12	US-08-843-530B-36	US-09-007-476-2	US-08-533-669A-10	US-08-607-509-2	US-08-607-509-4	US-08-454-036-2	US-08-634-642-2	US-08-634-642-4	US-08-989-370-2	US-08-989-370-4	PCT-US95-05064-2	US-08-846-762-85	US-08-553-436A-6	PCT-US92-00282-5	US-08-853-948B-2	US-08-766-014-4	US-08-766-014-3	US-08-356-354-2	US-08-778-656-2
	DB	7	7	7	4	2	7	-	2	7	4	7	0	7	7	7	7	٣	m	2	7	7	Ŋ	4	1	-	7	7
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dР	Query	6.0	5.7	5.7	5.7	5.6	5.5	5.5	5.5	5.4	5.2	5.1	5.1	5.1	5.1	5.1	5.1	5.1	5.1	5.1	5.0	5.0	5.0	5.0	4.9	4.9	4.9	4.9
	Score	117.5	112.5	112.5	112.5	110	108	108	108	105.5	102.5	101	101	101	101	101	101	101	101	101	66	66	98	98	97.5	97.5	96.5	96.5
	Result No.		7	က	4	'n	9	7	80	6	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	26	27

qq

Sequence 2, Appli	Sequence 4, Appli	Sequence 4, Appli	Sequence 3, Appli	Sequence 2, Appli	Sequence 2, Appli	Patent No. 5213972	Sequence 6, Appli	و	Sequence 6, Appli	9	9	Sequence 32, Appl	Sequence 8, Appli	Sequence 4, Appl1	2	Sequence 70, Appl	Sequence 8, Appli
US-08-766-014-2	US-08-356-354-4	US-08-778-656-4	PCT-US92-00282-3	US-08-446-855A-2	US-09-150-741-2	5213972-7	US-08-356-354-6	US-08-778-656-6	PCT-US92-00282-6	US-08-097-829-6	US-08-577-403-6	US-08-843-530B-32	US-08-717-515-8	US-08-717-515-4	US-08-630-822A-70	US-09-005-069-10	US-08-090-523-8
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872	1054	1054	533	2391	2391	241	806	806	531	207	507	751	1276	876	586	586	521
4.9	4.8	4.8	4.8	4.7	4.7	4.7	4.7	4.7	4.7	4.6	4.6	4.6	4.6	4.6	4.5	4.5	4.5
96.5	95.5	. 95.5	94	93.5	93.5	92.5	92.5	92.5	92	90.5	90.5	90.5	90.5	06	83	83	88
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IMGN----RDDIDDMSAGNASVLTTVLKLIDKYDLYGSVAFPKHHNQADVPEIYRLAAKM 580
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        125 GRVIPTFNVM---TDFCLHKIWVHENVDKYYVATDYVKEKLLEI-GTHPSNVKITGIPIR 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PQFEESM-----PVGPIYKKYNLSPNKKVLLIMAGAHGVLKNVKELCENLVKDDQVQVVV 235
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ---ELFRITDCM 277
Length 1068;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               87; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                OPERATING SYSTEM: PC_DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/718,777
FILING DATE: NOT YET ASSIGNED
CLASSIFICATION: 800
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/175,471
FILING DATE: 27-DEC-1993
FILING DATE: Z7-DEC-1993
ATTORNEY/AGENT INFORMATION:
NAME: Barbara Ree-Venter
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      5.7%; Score 112.5; DB 2;
20.9%; Pred. No. 0.012;
iive 56; Mismatches 87;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         2: Law Offices of Barbara Rae-Venter
260 Sheridan Avenue, Suite 440
                                                                                                                                                                                                                                                                                                                                                                     MODIFICATION OF SUCROSE PHOSPHATE SYNTHASE IN PLANTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            236 VCGKNTALKESLSALEAENGDKL-KVLGYVERID---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CGNE.072.02US
                                                                                                      636 IADALLKLVADKNLWQECRRNGLRNIHL 663
                                                               328 ILESVTSLLADEDTLHRMKKN-IKDLHL 354
                                                                                                                                                                                                            Sequence 7, Application US/08718777
Patent No. 5981852
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NAME: Barbara Rae-Venter
REGISTRATION NUMBER: 32,750
REFERENCE/DOCKET NUMBER: CGI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         E: Floppy disk
IBM PC compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TELECOMMUNICATION INFORMATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 INFORMATION FOR SEO ID NO: 7 SEQUENCE CHARACTERISTICS:
LENGTH: 1068 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (415)328-4400
                                                                                                                                                                                                                                                                     Van Assche, C.
Lando, D.
Bruneau, J. M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match 5.7%
Best Local Similarity 20.9%
Matches 56; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (415)328-4477
                                                                                                                                                                                                                                                                   APPLICANT: Van Assche,
APPLICANT: Lando, D.
APPLICANT: Bruneau, J.)
APPLICANT: Woelker, T.
APPLICANT: Gervais, M.
TITLE OF INVENTION: MOD
TITLE OF INVENTION: PHOD
TITLE OF INVENTION: SYN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ; MOLECULE TYPE: protein US-08-718-777-7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                      NUMBER OF SEQUENCES: 1
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Palo Alto
California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    amino acid
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ADDRESSEE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COUNTRY:
                                                                                                                                                                       RESULT 3
US-08-718-777-7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STREET:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STATE:
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                                                                                                        qq
                                                                              Sequence 11, Application US/08429054A

Patent No. 5917126

GENERAL INFORMATION:
APPLICANT: VAN ASSCHE, CHARLES; LANDO, DANIELLE; BRUNEAU,
APPLICANT: JEAN; VOELKER, TONI; GERVALS, MONICA
APPLICANT: JEAN; VOELKER, TONI; GERVALS, MONICA
TITLE OF INVENTION: SUCROSE PHOSPHATE SYNTHETASE (SPE),
TITLE OF INVENTION: A PREPARATION METHOD AND CDNA THEREFOR, AND USE OF THE
TITLE OF INVENTION: CDNA FOR MODIFYING SPS EXPRESSION IN PLANT CELLS
NUMBER OF SEQUENCES: 37
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                14;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 474 PIWAEVMRFLTNPHKPMILALSRPDPKKNITTLVKAFGECRPLREL------ANLTL 524
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 842,337
ETLING DATE: 20-March-1992
APPLICATION NUMBER: PCT/FR 91/00593
FILING DATE: 18-July-1991
CLASSIFICATION 600
PRIOR APPLICATION DATA:
APPLICATION NUMBER: French 90402094.9
FILING DATE: 20-July-1990
CLASSIFICATION: 800
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    56; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            26-APR-1995
18: 800
19: 800
                                                                                                                                                                                                                                                                                                                                                                                               ZIP: 10016
COMPUTER READABLE FORM:
MEDIUM TYPE: FLOPPY DISK
COMPUTER: IBM PC COMPATIBLE
COMPUTER: WORDPERFECT 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/429,054P
                                                                                                                                                                                                                                                                                             E: BIERMAN AND MUSERLIAN 600 THIRD AVENUE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NAME: Charles A Muserlian
REGISTRATION NUMBER: 19,683
REFERENCE/DOCKET NUMBER: 14
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TELEPHONE: (212) 661-8000
TELEFAX: (212) 661-8002
INFORMATION FOR SEQ ID NO: 11:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity 20.9
Matches 56; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MOLECULE TYPE: Peptide
                                                                                                                                                                                                                                                                            CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TYPE: Amino acid
STRANDEDNESS: Sinc
TOPOLOGY: Unknown
                                                                                                                                                                                                                                                                                                                                         CITY: NEW YORK STATE: NEW YORK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FILING DATE: 26
CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                    USA
                                                                                                                                                                                                                                                                                                 ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                US-08-429-054A-11
                                                                   US-08-429-054A-11
                                                                                                                                                                                                                                                                                                                                                                                  COUNTRY:
                                                                                                                                                                                                                                                                                                                       STREET:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               278
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S81 KGVFINPALVEPFGLTLIEAAAHGLPIVATKNGGPVDITNA----LUNGLLVDPHDQNA 635
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       127 VIPTE-----NVMIDFCLHKIWVHENVDKYYV-ATDYVKEKLLEIGTHPSNVKITG 176
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    H-TFPGRLANFIANILENYLYHCLY----SKYEILASDLLKRDVSLPALHQNSLWLLR 253
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            254 YDF--VERYPRPVMPNMIFIGGINCKKKGNLSQEFEAYVNASGEHGIVVFSLGSMVSEIP 311
                                        ---ITKPGGITLTEATAIGVPVILYKPVPGQEKENANFFEDRGAAIVVNRHEE-- 327
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           -----YRGVDKIYNKRKFNIYFKMGNKRLGELVDEHQPDIIINTFPMIVVPEYRRTGR 126
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20.5%; Pred. No. 0.0071;
.ive 57; Mismatches 137; Indels 112;
                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 7, Application PC/TUS9200282
GENERAL INFORMATION:
APPLICANT: OWENS, IDA S.
APPLICANT: RITHE, JOSEPH K.
TITLE OF INVENTION: THE GENETIC LOCUS UGT1 AND A MUTATION
TITLE OF INVENTION: THEREIN.
NUMBER OF SEQUENCES: 40
CORRESPONDENCE ADDRESS:
ADDRESSEE: CUSHMAN DARBY & CUSHMAN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      --LYLK----SFSIGKQFYRLF-
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SOFTWARE: Patentin Release #1.0, Version #1.25
SOFTWENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US92/00282
FILING DATE: 19920110
CLASSIFICATION: 435
CLASSIFICATION: 435
NAME: SCOTT, WATSON T.
REGISTRATION NUMBER: 26581
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ADDRESSEE: CUSHMAN DARBY & CUSHMAN STREET: 1615 L STREET, N.W. CITY: WASHINGTON
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IADALLKLVADKNLWQECRRNGLRNIHL 663
                                                                                                                                                                                 328 ILESVISLLADEDILHRMKKN-IKDLHL 354
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ZIP: 20036-5601
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-661-3000
TELEFAX: 202-622-0944
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INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
LENGTH: 529 amino acids
TYPE: AMINO ACID
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Best Local Similarity 20.5
Matches, 79; Conservative
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PCT-US92-00282-7
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-----ITKPGGITLTEATAIGVPVILYKPVPGQEKENANFFEDRGAAIVVNRHEE-- 327
                                                581 KGVFINPALVEPFGLTLIEBAAAHGLPIVATKNGGPVDITNA-----LNNGLLVDPHDQNA 635
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        125 GRVIPTFNVM---TDFCLHKIWVHENVDKYYVATDYVKEKLLEI-GTHPSNVKITGIPIR 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         POFEESM-----PVGPIYKKYNLSPNKKVLLIMAGAHGVLKNVKELCENLVKDDQVQVVV 235
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      474 PIWAEVMRFLTNPHKPMILALSRPDPKKNITTLVKAFGECRPLREL-----ANLTL 524
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 --ELFRITDCM 277
                                                                                                                                                                                                                                                                                                                                                                             Sequence 7, Application US/09051341
Patent No. 6124528
GENERAL INFORMATION:
APPLICANT: Shewmaker, C. K.
TITLE OF INVENTION:
SUCROSE PHOSPHATE SYNTHASE ENCODING SEQUENCE
TITLE OF INVENTION: SUCROSE PHOSPHATE SYNTHASE ENCODING SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 1068;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA: APPLICATION NUMBER: US/09/051,341
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match. 5.7%; Score 112.5; DB 4; Best Local Similarity 20.9%; Pred. No. 0.012; Matches 56; Mismatches 87;
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ER: CGNE.110.02US
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NUMBER OF SEQUENCES: 14
COORRESPONDENCE ADDRESS:
ADDRESSEE: Rae-Venter Law Group, P.C.
STREET: 260 Sheridan Avenue, Suite 440
CITY: Palo Alto
STATE: California
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CLASSIFICATION: 800
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/US96/17351
FILING DATE: 25-OCT-1996
APPLICATION NUMBER: US 08/549,016
FILING DATE: 27-OCT-1995
PRIOR APPLICATION DATA: US 08/372,200
FILING DATE: 12-JAN-1995
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          236 VCGKNTALKESLSALEAENGDKL-KVLGYVERID
                                                                                                                                        328 ILESVTSLLADEDTLHRMKKN-IKDLHL 354
                                                                                                                                                                                 | ::: |:||:|| |:|| |:::|| |:::|| |:::|| |:::|| |:::|| |:::|| |:::|| |:::|| |:::|| |:::|| |:::|| |:::|| |:::|| |:::|| |:::|| |:::|| |:::|| |:::|| |:::|| |:::|| |:::|| |:::|| |:::|| |:::|| |:::|| |:::|| |:::|| |:::|| |:::|| |:::|| |:::|| |:::|| |:::|| |:::|| |:::|| |:::|| |:::|| |:::|| |:::|| |:::|| |:::|| |:::|| |:::|| |:::|| |:::|| |:::|| |:::|| |:::|| |:::|| |:::|| |:::|| |:::|| |:::|| |:::|| |:::|| |:::|| |:::|| |:::|| |:::|| |:::|| |:::|| |:::|| |:::|| |:::|| |:::|| |:::|| |:::|| |:::|| |:::|| |:::|| |:::|| |::|| |:::|| |:::|| |:::|| |:::|| |:::|| |:::|| |:::|| |:::|| |:::|| |::|| |:::|| |:::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |:|| |:|| |:|| |::|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TELECOMMUNICATION INFORMATION:
TELEPHONE: (415)328-4400
IELEFAX: (415)328-4477
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERIZIES:
LENGTH: 1068 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ; MOLECULE TYPE: protein US-09-051-341-7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     amino acid
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                                                                                                                                                                                                                                                                                                                                                US-09-051-341-7
278
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216 -KNVKELCENLVKDDQVQVVVVCG-----KNTALKESLSALEAENGDKLKVLGYVERI 267
                                                                                   268 DELFRITDCMITKPGGITLTEATAIGVPVILYKPVPGQEKENANFFEDRGAAIVVNRHEE 327
                                                                                                              312 EKKAMEIAEALGRIPQTLLWRYTGTRPSNLAKNTILVKWLPQND------LLGHPK-- 361
                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: Gelfand, David H.
APPLICANT: Abramson, Richard D.
TITLE OF INVENTION: 5' TO 3' EXONUCLEASE MUTATIONS OF
TITLE OF INVENTION: THERMOSTABLE DNA POLYMERASES
NUMBER OF SEQUENCES: 38
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRIOR APPLICATION DATA:

APPLICATION NOWBER: US 063,509
PRIOR APPLICATION NOWBER: US 063,509
PRIOR APPLICATION DATA:
APPLICATION NOWBER: US 899,24Î
FILING DATE: 22-4UG-1986
PROR APPLICATION NOWBER: US 746,121
FILING DATE: 15-4UG-1991
PRIOR APPLICATION NOWBER: WO PCT/US90/07641
FILING DATE: 21-DEC-1990
PRIOR APPLICATION NOWBER: WO PCT/US90/07641
FILING DATE: 21-DEC-1990
PRIOR APPLICATION NOWBER: US 585,471
PRIOR APPLICATION NOWBER: US 585,471
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CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/977,434
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION UNBER: US 590,490
PRIOR APPLICATION NUMBER: US 590,466
FILING DATE: 28-SEP-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 590,466
FILING DATE: 28-SEP-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 590,213
FILING DATE: 28-SEP-1990
PRIOR APPLICATION NUMBER: US 53,394
FILING DATE: 15-MAY-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 513,441
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     3: Hoffmann-La Roche Inc
340 Kingsland Street
                                                                                                                                                                       328 ILESVTSLLADEDTLHRMKKNIKDL 352
                                                                                                                                                                                                                  415 TADDLENALKTVINNKSYKENIMRL 439
                                                                                                                                                                                                                                                                                                                        Sequence 12, Application US/07977434 Patent No. 5466591 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICATION NUMBER: US 143,441 FILING DATE: 12-JAN-1988
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICATION NUMBER: US 455,611
FILING DATE: 22-DEC-1989
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    US 609,157
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STREET: 340 Kingsland Street CITY: Nutley STATE: New Jersey ZIP: O7110-1199 COMPUTER READABLE FORM: COMPUTER: Macintosh OPERATING SYSTEM: 7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRIOR APPLICATION DATA:
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|----PLIDVLSEMELNGVYFDE 515
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            201 NKKVLLIMAGAHGVLKNVKELCENLVKDDQVQVVVVCGKNTALKESLSALEAENGDKLKV 260
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          87 IYFKMGNKRLGELVDEHQPDIIINTFPMIVVPEYRRTGRVIPTFNVMTDFCLHKIWVHE 146
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            261 LGYVE------RIDELFRITDCMITKPGGITLTEATAIGVPVILYKPVPGQEKEN 309
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       605 T-YIDSIPLSINRKTNRVHTTFHQTG---TSTGRLSSSNPNLQNLPT---RSEEGKEIRK 657
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  310 ANFFEDRGAAIVVNRHEEI-LESVTSLLADEDTLHRMKKNIKDLHLANSSEVILEDILKE 368
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  32 LGFQHVTVSNLYQESNPIVSEVTQYLYLK----SFSIGKQFYRLFYYGVDKIYNKRKFN &6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            147 NV-----DKYYVATDYVKEKLLEIGTHPSNVKITGIPIRPQFEESMPVGPI-YKKYNLSP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match 5.5%; Score 108; DB 1; Length 892; Best Local Similarity 19.4%; Pred. No. 0.026; Matches 72; Conservative 63; Mismatches 135; Indels 102;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GENERAL INFORMATION:

APPLICANT: Gelfand, David H.

APPLICANT: Gelfand, David H.

APPLICANT: Abramson, Richard D.

TITLE OF INVENTION: 5' TO 3' EXONUCLEASE MUTATIONS OF

TITLE OF INVENTION: THERMOSTABLE DNA POLYMERASES

NUMBER OF SEQUENCES: 38

CORRESPONDENCE ADDRESS:

ADDRESSEE: Hoffmann-La Roche Inc.

STREET: 340 Kingsland Street
                                                                                                                             NAME: Luann Cserr
REGISTRATION UNBER: 31,822
REFERENCE/DOCKET NUMBER: Case No. 5466591 8753
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FILING DATE: 02-NOV-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 557,517
FILING DATE: 24-JUL-1990
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 12, Application US/08458819
Patent No. 5795762
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STREET: 340 Kingle
CITY: Nutley
STATE: New Jersey
ZIP: 07110-1199
COMPUTER READABLE FORM:
MEDIUM IYPE: Floppy disk
AMOUNTORN
7
                                                                                                                                                                                                                               TELEPHONE: (510) 814-2972
INFORMATION FOR SEQ ID NO: 12:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WordPerfect 2.1
                                                                                                                                                                                                                                                                                                             LENGTH: 892 amino acids TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                  ; MOLECULE TYPE: protein US-07-977-434-12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    369 SEMMTAKOKAKV 380
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712 SEMFVSEQMRRV 723
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OPERATING SYSTEM:
SOFTWARE: WordPer
                                                                                                                                                                                                                                                                                                                                                               linear
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261 LGYVE------RIDELFRITDCMITKPGGITLTEATAIGVPVILYKPVPGQEKEN 309
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                                                                                                                                                                                                                                                                                    | | | ::| |::|
----NSSTQVAYILFEKLNIAP 564
                                                                            201 NKKVLLIMAGAHGVLKNVKELCENLVKDDQVQVVVVCGKNTALKESLSALEAENGDKLKV 260
                                                                                                                          -----LEYRKYQKLKS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 12, Application PC/TUS9107035
GENERAL INFORMATION:
APPLICANT: Gelfand, David H.
APPLICANT: Abramson, Richard D.
TITLE OF INVENTION: 5' TO 3' EXONUCLEASE MUTATIONS OF
TITLE OF INVENTION: 1' THERMOSTABLE DNA POLYMERASES
NUMBER OF SEQUENCES: 38
CORRESPONDENCE ADDRESS:
ADDRESSEE: Cetus Corporation
STREET: 1400 Fifty-third Street
                                                                                                                      565 YKKT-----ATGKFSTNAEVLEELSKEHEIAKLL---
             WO PCT/US90/07641
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STREET: 1400 Fifty-third Street CITY: Emeryville STRYEE: California ZIP: 94608
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SOFTWARE: WordPerfect 5.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US91/07035
FILING DATE: 19910930
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PILING DATE: 1991093 CLIASSIFICATION: 435
PRIOR PAPLICATION DATA:
APPLICATION NUMBER: US 590,490
FILING DATE: 28-SEP-1990
PRIOR PAPLICATION DATA:
APPLICATION NUMBER: US 590,466
FILING DATE: 28-SEP-1990
PRIOR PAPLICATION DATA:
APPLICATION NUMBER: US 590,213
FILING DATE: 28-SEP-1990
FILING DATE: 28-SEP-1990
FILING DATE: 15-SEP-1990
PRIOR APPLICATION NUMBER: US 523,394
FILING DATE: 15-MAY-1990
PRIOR APPLICATION NUMBER: US 143,441
FILING DATE: 12-JAN-1988
PRIOR APPLICATION NUMBER: US 143,441
FILING DATE: 12-JAN-1988
PRIOR APPLICATION NUMBER: US 053,509
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WordPerfect 5.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TS-AUG-1991
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    22-AUG-1986
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     17-JUN-1987
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FILING DATE: 17-JUN-
PRIOR APPLICATION DATA:
APPLICATION NUMBER: U
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PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRIOR APPLICATION DATA: APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                       |||| ::| :|
712+SEMFVSEQMRRV 723
                                                                                                                                                                                                                                                                                                                                             369 SEMMTAKOKAKV 380
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         87 IYFKMGNKRLGELVDEHQPDIIINTFPMIVVPEYRRTGRVIPTFNVMTDFCLHKIWVHE 146
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       63; Mismatches 135; Indels 102;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           5.5%; Score 108; DB 1; Length 892; 19.4%; Pred. No. 0.026;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      431 LGYKMISFDELVNENVPLFGNDFSYVPLERAVEYSCEDADVTYRIF----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            REFERENCE/DOCKET NUMBER: Case NO. 5795762 8753 TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICATION NUMBER: WO PCT/US90/07641
02-JUN-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICATION NUMBER: ...
FILING DATE: 21-DEC-1990
PRIOR APPLICATION NUMBER: US 585,471
FILING DATE: 20-SEP-1990
PRIOR APPLICATION DATA:
                                                                                          PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/977,434
FILING DATE: 23-FEB-1993
APPLICATION NUMBER: US 590,490
FILING DATE: 28-SEP-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 590,466
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ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                            APPLICATION NUMBER: US 590,466
FILING DATE: 28-SEP-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 590,213
FILING DATE: 28-SEP-1990
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICATION NUMBER: US 143,441
FILING DATE: 12-JAN-1988
FILING DATE: 12-JAN-1988
APPLICATION NUMBER: US 063,509
FILING DATE: 17-JUN-1987
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 899,241
FILING DATE: 22-AUG-1986
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 746,121
FILING DATE: 15-AUG-1991
PRIOR APPLICATION DATA:
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PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 609,157
FILING DATE: 02-NOV-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 557,517
                                                                                                                                                                                                                                                                                                                                                                US 523,394
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REGISTRATION NUMBER: 31,822
                                                                                                                                                                                                                                                                                                                                                              APPLICATION NUMBER: US 52
FILING DATE: 15-MAY-1990
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TELEPHONE: (510) 814-2972
INFORMATION FOR SEQ ID NO: 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     22-DEC-1989
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity 19.49
Matches 72; Conservative
         CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ) MOLECULE TYPE: protein US-08-458-819-12
                                                                       CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TOPOLOGY:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     111 TFPMIVVPEYRRRTGRVIP----TFNVMTDFCLHKIWVHENVDKYYVATDYVKEKLLEIG 166
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     167 THPS------NVKITGIPIRPQFE-----ESMPVGPIYKKYNLSPNKKVLLIMA 209
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           210 GAHGVLKNVKELCENLVKDDQVQVVVVCGKNTALKESLSALEAENGDKLKVLGYVERIDE 269
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    270 LFRITDC------XITKPGGITLTEAT-----AIGVPVIL-----XK 300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 47 TSNYKNLRSDRLYIAAQLKSSQI-----DQTLNYLYYQAYYLASRDALQSSLTSYVAGNK 101
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    195 ANPSIILTDSRVYGYITIIMSAEGLKSVFNDTTALEHSTIAIISAVYNSQGKASGYHFVF 254
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                11 TANYGN --- GHVQVAKTLYEQCVRLGFQHVTVSNLYQES-----NPIVSEVTQYL----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Indels 117;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 1220;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 2, Application US/09007476
Patent No. 6159949
GENERAL INFORMATION:
GENERAL INFORMATION:
TITLE OF INVENTION: No. 6159949el FtsY
NUMBER OF SEQUENCES: 2
CORRESPONDENCES: 2
CORRESPONDENCE ADDRESSE: Dechert Price & Rhoads
STREET: 4000 Bell Atlantic Tower, 1717 Arch Stre
                                                                                                                                                                                                               OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match 5.4%; Score 105.5; DB 2; Best Local Similarity 20.2%; Pred. No. 0.076; Matches 76; Conservative 60; Mismatches 124;
                                                                                                                                                                                                                                                                                                                                                                                                                                                     REGISTRATION NUMBER: 38,230
REGISTRATION NUMBER: 0TC-02717
RELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 307-8410
TELEPHONE: (415) 307-8438
INFORMATION FOR SEQ ID NO: 36:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                         FILING DATE: 16-APR-1997
CLASSIECATION: 435
California : United States of America
                                                                                                                          MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SS: not relevant not relevant
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LENGTH: 1220 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                           ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             301 PVPGQEKENANFFEDRG 317
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    360 PIVRLQKATELITEGRG 376
                                                                          ZIP: 94104
COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ; MOLECULE TYPE:
US-08-843-530B-36
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         US-09-007-476-2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               15;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          87 IYFKMGNKRLGELVDEHQPDIIINTFPMIVVPEYRRTGRVIPTFNVMTDFCLHKIWVHE 146
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        147 NV-----DKYYVATDYVKEKLLEIGTHPSNVKITGIPIRPQFEESMPVGPI-YKKYNLSP 200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 201 NKKVLLIMAGAHGVLKNVKELCENLVKDDQVQVVVVCGKNTALKESLSALEAENGDKLKV 260
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              261 LGYVE------RIDELFRITDCMITKPGGITLITEATAIGVPVILYKPVPGQEKEN 309
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  T-YIDSIPLSINRKTNRVHTTFHQTG---TSTGRLSSSNPNLQNLPT---RSEEGKEIRK 657
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AVRPQRQDWWILGADYSQIELRVLAHVSKDENLLKAFKEDL-DIHTITAAK----IFGV 711
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                565 YKKT-----ATGKFSTNAEVLEELSKEHEIAKLL------LEYRKYQKLKS 604
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   310 ANFFEDRGAAIVVNRHEEI-LESVTSLLADEDTLHRMKKNIKDLHLANSSEVILEDILKE 368
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              32 LGFQHVTVSNLYQESNPIVSEVTQYLYLK-----SFSIGKQFYRLFYYGVDKIYNKRFN 86
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 5.5%; Score 108; DB 5; Length 892;
19.4%; Pred. No. 0.026;
ative 63; Mismatches 135; Indels 102;
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APPLICANT: Agnan, Jacqueline
APPLICANT: Alex, Lisa A.
APPLICANT: Simon, Melvin I.
TITLE OF INVENTION: Osmosensing Histidine Kinases
NUMBER OF SEQUENCES: 36
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STREET: 220 Montgomery Street, Suite 2200
                                                                                                                                                                                                                                                                                                                                                                                                                                                             Case No. 2580
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                                                                                                                                                               APPLICATION NUMBER: US 609,157
FILING DATE: 02-NOV-1990
PRICA APPLICATION DATA:
APPLICATION NUMBER: US 557,517
FILING DATE: 24-JUL-1990
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                         REGISTRATION NUMBER: 32,630
REFRENCE/DOCKET NUMBER: Case
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-420-3300
INFORMATION FOR SEQ ID NO: 12:
SEQUENCE CHARACTERISTICS:
LENGTH: 892 amino acids
TYPE: AMINO ACID
                                                                                                                                                                                                                                                                                                                                                                                          Sias Ph.D, Stacey R. RATION NUMBER: 32,630
                  PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 45
FILING DATE: 22-DEC-1989
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match 5.5%
Best Local Similarity 19.4%
Matches 72; Conservative
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MOLECULE TYPE: protein

PCT-US91-07035-12
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Sequence 2, Application US/08607509
Patent No. 5876735
GENERAL INFORMATION:
GAPLICANT: Reed, Steven G.
TITLE OF INVENTION: METHODS FOR ENHANCEMENT OF PROTECTIVE IMMUNE RESPONSES
NUMBER OF SEQUENCES: 15
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    75 GKTGAFSIGLLQRLDFRHNLIQGLV----LSPTRELALQTAEVISRIGEFLSNSAKFCE 129
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              168 HPSNVKITGIPIRPQFEESMPVGPIYKKYNLSPNKKVLL----IMAGAHGVLKNVKELCE 223
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  224 NL-----VKDD----QVQVVVVCG------KNTALK-ESLSALEAENGDKLKVLGYV 264
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            265 ERIDELFRITDCMITKPGGITLTEATAIGVPVILYKPVPGQEKENANFFEDRGAAIVVNR 324
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     190 DQIXEIFR----FLPKDIQVALFSAT------MPEEVLELTKKFMRDPVRILVKR 234
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           23 RPIPSFDDMP------LHQNLLRGIYSYGFEKPSSIQQRAIAPFTRGGDIIAQAQSGT 74
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     325 HEEILESVTSLLADEDTLHRMKKNIKDLH--LANSSEVILEDILKESEMMTAK 375
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     235 ESLTLEGIKQFFIAVEEEHKL-DTLMDLYETVSIAQSVIFANTRRKVDWIAEK 286
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 403;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/607,509 FILIGN DATE: 16-FEB-1996 CLASSIFICATION: 435
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEED and BERRY LLP 5300 Columbia Center, 701 Fifth Avenue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          5.1%; Score 101; DB 2; L. Local Similarity 20.8%; Pred. No. 0.04; nes 61; Conservative 50; Mismatches 110;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        126 RVIPTFNVMTDFCLHKIWVHENVDKYYVATDYVKEKLL----
                                                                     APPLICATION NUMBER: US/08/533,669A
FILING DATE: 22-SEP-1995
CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: MAXi, David J.
REGISTRATION NUMBER: 31,392
REFERENCE/DOCKET NUMBER: 210121.420
TELECOMMUNICATION INFORMATION:
TELECHNONE: (206) 622-4900
TELECRAX: (206) 682-6031
INFORMATION FOR SEQ ID NO: 10:
SEQUENCE CHÂRACTERISTICS:
LENGTH: 403 amino acids
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COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARR: Patentin Release #1.0,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FILING DATE: 16-FEB-1996
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Maki, David J.
                                                                                                                                                                                                                                                                                                                                                                                                   TOPOLOGY: linear

MOLECULE TYPE: protein

US-08-533-669A-10
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ZIP: 98104-7092
COMPUTER READABLE FORM:
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STATE: Washing
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ADDRESSEE:
STREET: 63
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      291 AIGVPVILYKPVP-GQEKENANFFEDRG-----AAIVVNRHEEI--LESVTSLLADEDTL 342
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   176 GIPIRPQFEESMPVGPIYKKYNLSPNKKVLLIMAGAHGVLKNVKELCENLVKDDQVQVVV 235
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 298 NRAVPDAPHEALLCLDATTGQ - - NALSQARNFKEVTNVTGIVLTKLDGTAKGGIVLAIRN 355
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         21;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       5.2%; Score 102.5; DB 4; Length 416; 24.5%; Pred. No. 0.029; tive 35; Mismatches 83; Indels 21
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Sequence 10, Application US/08533669A

Sequence 10, Application US/08533669A

Sequence 10, Application US/08533669A

GENERAL INFORMATION:

APPLICANT: COTIXA COTPORATION

TITLE OF INVENTION: THERAPY AND DIAGNOSIS OF LEISHMANIASIS

NUMBER OF SEQUENCES: 18

CORRESPONDENCE ADDRESS:

ADDRESSEE: SEED and BERRY LLP

STREET: 6300 Columbia Center, 701 Fifth Avenue
                                                                                                                                      COMPUTER: IBM COMPATIBLE
OPERATING SYSTEM: DOS
SOFTWARE: FastSEG for Windows Version 2.0
CURRENY APPLICATION DATA:
APPLICATION NUMBER: US/09/007,476
                                                                                                                                                                                                                                                                                                                                                                                                                                                       GM10079
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
                                                                                                                                                                                                                                                                                                                                                                                                                              36,795
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TELECOMMUNICATION INFORMATION:
TELEPHONE: 215-994-248
TELEFAX: 215-994-2222
                                                                                                                                                                                                                                                                                 CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Falk, Stephen T
REGISTRATION NUMBER: 36,79
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    information for SEQ ID NO: 2: SEQUENCE CHARACTERISTICS: LENGTH: 416 amino acids TYPE: amino acid STRANDEDNESS: single STRANDEDNESS: single US-09-007-476-2
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Best Local Similarity 24.54
Matches 45; Conservative
                                                                                                                         Diskette
                                                                                         COMPUTER READABLE FORM
  Philadelphia
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STATE: Washington
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ZIP: 98104-7092
                                                                                                                       MEDIUM TYPE:
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NUMBER OF SEQUENCES: COMPOUNDS AND METHODS FOR THE STIMULATION AND ENHANCEMENT O CORRESPONDENCE ADDRESS: ADDRESSE: SEED and MEDEW.
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                                                                                                                                                                       Gaps
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                                                                                                                              Length 403;
                                                                                                                            ; Score 101; DB 2; Length 403; Pred. No. 0.04; 51; Mismatches 110; Indels
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MEDIUM TYPE: Floppy disk
GOMPUTER: IBM PC compatible
OPPRATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
RPPLICATION NUMBER: US/08/454,036
FILING DATE: 30-MAY-1995
CLASSIFICATION: 514
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            E: SEED and BERRY 6300 Columbia Center, 701 Fifth Avenue
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Patent No. 5876966
GENERAL INFORMATION:
APPLICANT: Reed, Steven G.
TITLE OF INVENTION: COMPOUNDS AN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   P-39,244
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ATTORNEY/AGENT INFORMATION:
NAME: Kadlecek, Ann T.
REGISTRATION NUMBER: P39,2
REFERBKCE/DOCKET NUMBER: 21
TELECOMMUNICATION INFORMATION:
                                                                                                                              5.1%;
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(206)682-6031
                                                                                                                 Ouery Match
Best Local Similarity 20.5%
Matches 60; Conservative
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                                      ; MOLECULE TYPE: protein US-08-607-509-4
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CITY: Sec.

STATE: Washing.c.

COUNTRY: USA

TO: 98104-7092
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TELEFAX: (
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TITLE OF INVENTION: METHODS FOR ENHANCEMENT OF PROTECTIVE IMMUNE RESPONSES
NUMBER OF SEQUENCE: 15
CORRESPONDENCE ADDRESS:
ADDRESSEE: SEED and BERRY LLP
STREET: 6300 Columbia Center, 701 Fifth Avenue
                                                                                                                                                                                                                                                                                                                                   12;
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                                                                                                                                                                                                                                                                                                                               50; Mismatches 110;
                                                                                                                                                                                                                                                                                                                                                                       126 RVIPTFNVMTDFCLHKIWVHENVDKYYVATDYVKEKLL---
                 REFERENCE/DOCKET NUMBER: 210121.404C3
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206) 622-4900
TELEFAX: (206) 682-6031
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
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APPLICATION NUMBER: US/08/607,509
FILING DATE: 16-FEB-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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Patent No. 5876735
GENERAL INFORMATION:
  31,392
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TELEFAX: (206) 682-6031
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
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NAME: Maki, David J.
                                                                                                                                             : 403 amino acids
amino acid
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REGISTRATION NUMBER:
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CITY: Seattle
STATE: Washington
COUNTRY: USA
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                                                                                                                                                                                                                                                                                                             Local Similarity
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                           Gaps
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                       Indels
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
APPLICATION NUMBER: US/08/634,642
FILING DATE: 18-APR-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NUMBER OF SEQUENCES: 15
CORRESPONDENCE, ADDRESS:
CORRESSEE: SEED and BERRY LLP
STREET: 6300 Columbia Center, 701 Fifth Avenue
                       110;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match 5.1%; Score 101; DB 2; I Best Local Similarity 20.8%; Pred. No. 0.04; Matches 61; Conservative 50; Mismatches 110;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: Reed, Steven G.
TITLE OF INVENTION: METHODS FOR ENHANCEMENT OF
TITLE OF INVENTION: PROTECTIVE IMMUNE RESPONSE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           126 RVIPTFNVMTDFCLHKIWVHENVDKYYVATDYVKEKLL----
                                                             126 RVIPTFNVMTDFCLHKIWVHENVDKYYVATDYVKEKLL-
Best Local Similarity 20.8%; Pred. No. 0.04
Matches 61; Conservative 50; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 2, Application US/08634642
Patent No. 5879687
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ATTORNEY/AGENT INFORMATION:
NAME: Maki, David J.
REGISTRATION NUMBER: 31,392
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TELEFAX: (206) 682-6031
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
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STATE: Washington
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Copyright (c) 1993 - 2000 Compugen Ltd.
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Maximum Match 100%
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                                                                                          OM nucleic - nucleic search, using sw model
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AX016297 Sequence X14770 Staphylococ AF270166 Staphyloc AF270394 Staphyloc AR106079 Sequence E35634 Mure. 2/200 AX016296 Sequence L77246 Bacillus su

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E35634 AX016296 BACYACA

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Description

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SUMMARIES

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Z99115 Bacillu	292859 Caenornabdı AL033123 Caenorhab AJ000331 Arabidops AF098501 Caenorhab AL034393 Caenorhab	AL008B71 Caenc AC010727 Homo AB047398 Arab: AX083744 Sequ	AL590063 HOMO AL391538 HOMO AC060805 HOMO AC023371 HOMO	AC084152 Caeno AF04464 Pieri. AL359196 Homo AL429890 clon	AC005506 Plas AC025184 Homo AB047399 Arab AF241797 Arab	AL403832 T3 e AC006487 Homo AC067973 Homo AC012627 Homo	AC021145 Homo AC008739 Homo AL142826 Anoph AC004153 Plasm	AL033123 Caenorhab AC004616 Homo sapi Z92859 Caenorhabdi AL411257 T7 end of	AL412260 T7 enc AL360177 Homo s AP000459 Homo	·	PAT 07-SEP-2000	stridium group; phylococcus.	and Wolter, F.P.  HENRINGER ULRICH (DE); HEINZ ERNST BRANK P. (DE): GVS GES FUER ERWERB		DB 9; Length 975; .5e-164; s 0; Indels 0; Gaps ggctcattcggtaacggtcatatg 60
12.1 213680 2 BSUB0012 29911	4 242893 83 CEYS3C12 2 1496 6 CEYS3C12D 9 1648 13 ATMGDGSYN 8 44352 6 CELH28G03 8 152878 6 CEYY8B10A	5.8 247332 83 CEY18D10 5.7 148061 87 AC010727 5.6 1574 12 AB047398 5.6 1141 10 AX083744	5.6 175415 82 AL590063 5.6 169437 81 AL391538 5.5 214631 72 AC060805 5.5 53932 68 AC023371	5.4 54345 4 ACO84152 5.4 1154 5 AFO44864 5.4 1189 80 AL359196 5.4 867 53 CNSO75BG	5.3 205429 60 AC005506 5.3 129388 69 AC025184 5.3 1775 12 AB047399 5.3 1929 13 AF241797	5.2 1038 53 CNSO66L7M 5.2 186625 86 ACO06487 5.2 155317 73 ACO67973 5.2 100925 87 AC012627	5.2 170432 67 AC022145 5.2 235532 87 AC008739 5.1 910 53 CNSOLG8P 5.1 156060 60 AC004153	5.1 1496 6 CEY53C12D 5.1 149752 85 ACO04616 5.1 242893 83 CEY53C12 5.1 759 53 CNSO6OXV	5.1 1013 53 CNSOGRPO 5.1 166331 80 AL360177 5.1 171863 91 AP000459	ALIGNMENTS	975 bp DNA PAT 07-SEP from Patent W09949052.	RSION AX016297.1 GI:10041860 WORDS Staphylococcus aureus. ORGANISM Staphylococcus aureus Bacteria; Firmfuctes; Bacillus/Clostridium group; Racillus/Staphylococcus aroub; Staphylococcus.	Jorasch, P. and Wolter, F. P. erase -SEP-1999; (DE); ZAEHRINGER ULRICH (DE); WOLTER FRANK P. (DE); GVS GES		Length 975; Indels 0; Ga cggtaacggtcatatg

BASE COUNT ORIGIN

RESULT 1
AX016297
LOCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM

REFERENCE AUTHORS TITLE JOURNAL

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MITKRGGITTITGSPRQDPKKYATQTICRDLDLIGHSSQPQEIYGKVPLYARFFVK"
1452 c 1130 g 2668 t 24 others
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   541 aacaaatttgaaacgcctattaatcaaaagcagtggttaatagacaacaacttagatcca
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.5150
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Best Local Similarity
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                                                                            Bacteria; Firmicutes, Bacillus/Clostridium group;
Bacillus/Staphylococcus group; Staphylococcus.

1 (bases 1 to 7791)
Ludovice,A.M., Wu,S. and de Lencastre,H.
Molecular cloning and DNA sequencing of the Staphylococcus aureus
UDP-N-acetylmuramyl tripeptide synthetase (murE) gene, essential
for the optimal expression of methicillin resistance
Microb. Drug Res. 4, 85-90 (1998)
Ludovice,A.M.
                                                                                                                                                                                                                                                                             Direct Submission
Submitted (30-JUL-1997) A.M. Ludovice, Instituto de Tecnologia
Qiomica e Biologica, Universidade Nova de Lisbon, R. da Quinta
Grande 6, Apartado 127, 2780 Oeiras, PORTUGAL
Revised by author 16-JAN-98
Related sequence: L77246.
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/protein_id="CAA74740.1"
          murb gene; peptide chain release factor 3; RF3 gene; UDP-N-acetylmuramyl-tripeptide synthetase; ypfP gene. Staphylococcus aureus. Staphylococcus aureus
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/protein_id="CAA74739.1"
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//organism="Staphylococcus aureus"
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/gene="RF3"
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complement(3009. .3013)
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/gene="murE"
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Bacteria; Firmicutes; Bacillus/Clostridium group;
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I (bases 1 to 3118)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Taylor, J. David, Kimmerly, W.J., Nelsen, A.J., Godlevski, M.M.,
Rubino, M.A., Nelson, F.J., Rivers, P.R., Torruella-Miller, I.,
Listenbee, S., Ashanti, C., Altshuller, G., Mamo, L., Shepherd, N.S.,
Fuchs, R., Fleming, T., Guan, X., Du, L., Cain, D.H., Miller, G.S. and
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Bacilus/Staphylococcus group; Staphylococcus.
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Kimmerly,W.J., Taylor,J.David, Nelsen,A.J., Godlevski,M.M.,
Kimmerly,W.A., Nelson,F.J., Rivers,P.R., Torruella-Miller,I.,
Listenbee,S., Ashanti,C., Altshuller,G., Mamo,L., Shepherd,N.S.,
Fuchs,R., Fleming,T., Guan,X., Du,L., Cain,D.H., Miller,G.S. and
                                                                                                                                                                                                                            Taylor,J.David, Kimmerly,W.J., Nelsen,A.J., Godlevski,M.M.,
Rubino,M.A., Nelson,F.J., Rivers,P.R., Torruella-Miller,I.,
Listenbee,S., Ashantl,C., Altshuller,G., Mamo,L., Shepherd, N.S.,
Fuchs,R., Fleming,T., Guan,X., Du,L., Cain,D.H., Miller,G.S. and
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Pred. No. 3.2e-104;
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Sequence 1 from Patent W09949052.
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PF 25-SEP-1997
US 60/059956,10-DEC-1997 US 08/988251 PI
NICOLA G WALLIS,LISA K SCHILLING, SUSAN ZABIRKOSUKI PC
C12N15/09, AG1K31/00, AG1K39/005, AG1K39/005, AG1K39/005, AG1K39/005, AG1K39/00, C12N15/00, C12N15
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SMITHKLINE BEECHAM CORP, SMITHKLINE BEECHAM CORP PUBLIC LTD CO
OS Unidentified
PN JP 1999225779-A-71
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1 (bases 1 to 2600)
Nicola, G.W.L.L. and Schilling, S.Z.
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/organism="unidentified"
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1 (bases 1 to 1149)
Zaehringer, U., Heilar, E., Jasch, P. and Wolter, F.P.
Zaehringer, U., Heilar, E., Jasch, P. and Wolter, F.P.
Processive glycosyltransferase
Patent: WO 9949052-A 1 30-SEP-1999;
FORSCHUNGSERTRUM BORSTEL (DE); ZAEHRINGER ULRICH (DE); HEINZ ERNST (DE); JORASCH PETRA (DE); WOLTER FRANK P (DE); GVS GES FUER ERWERB UND VERWER (DE)
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Bacteria; Firmicutes; Bacillus/Clostridium group;
Bacillus/Staphylococcus group; Bacillus.
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48.5%; Pred. No. 7.6e-12;
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Bacillus subtilis (YAC10-9 clone) DNA region between the serA and
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                                                                                                        364 CGCCGAACTGGAAGAGTCATTCCTACCTTCAACGTTATGACTGATTTTTGTCTTCATAAA
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                                                                                                                                                                                                                                                                                                                         364 gagcaatttaacattaatattccagttgctacagtgatgacagactatcgcttacataaa
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Chromosome
Microbiology (1996) In press
3 (bases I to 35040)
Capuano, V., Galleron, N., Pujic, P., Sorokin, A.V. and Ehrlich, S.D.
Capuano, V., Galleron, N., Pujic, P., Sorokin, A.V. and Ehrlich, S.D.
Organization of the Bacillus subtilis chromosome between kdg and
the attachment site of the SPbetta prophage - use of Long Accurate
PCR and yeast artificial chromosomes for sequencing
mnoublished (1996)
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FRANGOTHYTIESSGIAMPANTGLKGVPVVPARRHKSLTLTDNLLTASVYSFTKQ
TESQIAMSTHLENDDHVLLIDDFLANGQAAHGLVSIVKQAGASIAGIGIVIEKSFQP
GRDELVKLGYRVESLARIQSLEEGKVSFVQEVHS"
                                                                                                                                dihydrofolate
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                                                                                                                                                                                                                                               Description, No., Azevedo, V., Zumstein, E., Galleron, N., Ehrlich, S.D. Sorokin, A.V., Azevedo, V., Zumstein, E., Galleron, N., Ehrlich, S.D. Sorokin, A.V., Azevedo, V., Zumstein, E., Galleron, S.D. Sequence analysis of the Bacillus subtilis chromosome region between the serA and kdg loci cloned in a yeast artificial
                          Baciilus/Staphylococcus group; Bacillus.

(bases 1 to 35040)

1 (bases 1 to 35040)

1 wakura,M., Kawata,M., Tsuda,K. and Tanaka,T.

Nucleotide sequence of the thymidylate synthase B and dihraductase genes contained in one Bacillus subtilis operon
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/product="adenine phosphoribosyltransferase"
/protein_id="AAA96611.1"
/db_xref="GI:1256617"
Bacteria; Firmicutes; Bacillus/Clostridium group;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /EC_number="2.4.2.7"
/function="purine blosynthesis"
/note="27% identity with E.coli adenine
phosphoribosyltransferase"
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1. .35040
/organism="Bacillus subtilis"
/sub_strain="168"
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/db_xref="G1:1256616"
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/map="205 degrees"
1. .1095
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/clone="YAC10-9"
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/citation=[3]
/codon_start=1
/transl_table=11
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/note="putative"
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/note="putative"
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88284366
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1426. .2010
/gene="xpt"
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<1. .1095
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/gene="ypaQ"
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/gene="xpt"
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LKEHTEMLKKDETGAPSFAEQLNIHTGLVQSLRDQLDEAEKÖMTEAEKRWQEEINRIL
KNNLITPERENELAAAFLESQEPSFKTGFFESKATRAQERDSKRNAFESDVAKRTEAE
ADMHNIDTJHKLAKYPDVTNESEKLIQAYREPLDISIIEHAVKHGARSSESVLQY
KDLAELIRKEAKREAADIIKVLSAMVKERVSKDVQTINDRLVQESEKLVFLQEQARLE
                                                                                                                          NIVAREKTDRIWAIWEEESACPWHIDTEWFKSKKTRVAAPEOKÖGRSOLTAQPMPKSEI
KWOGWALDOOLKRFYTLSDILGECSMLLKOTSAFREPKREEKKFLEERKFTALFGERSSG
KSSFANALVGERVLESSTPTTATINKITKPINGNITAANVVFKTANVVFKTEDDLAETLÛLI
GIPKEPAGRSFFEKWEKAVKKNILÖEBUVKLISNFLLAYEKYOOYIOEOKKLIFPLS
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ELKEIKSPKOFFEQKGKATFIEAVRWKLTKITEAWIKNEEESLISHYTAHLRRLQEDM
GEKAIAQITDQKETYLRGYAEGEHAKEIEMAYQACISWKNSDNTIKM"
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FFYMTYYQHSFSKGDRSFLRKLGLVKESLSMDKMFFIINAADLAKDKTELETVTDYVS
                                                                                                                                                                                                                                                                                           AELVKEGVYEPQLFTVSSKEELVGKPESFYNQFSKVRKHLDRFIEVDVKKASAAQLSS
EADKLCETVFQLHQSQHQSREEKEAQKQCLMLSFERTAADIEKRRNSKTIIEKVKKDT
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                                                                                                                                                                                                                                                                                                                                                       REQLYHIAQRLSYFANDLLKSAFHPGLQNGDWKKNVSKAMTTALHEYLFEYIQEIKTL
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Pred. No. 5.5e-12;
0; Mismatches 465; Indels
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9565. .10455
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/gene="ypbs"
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/gene="ypbs"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               KVEAVFFVSSTGLSTPSTEARLMINELPFSPYTKRIPINGLGCAGGASGLARABEYCKA
YPEAFVLVISAELCSLTFQPEDKTKRNLIGTSLFGDGIAAALLCGEKADRRYSKLKLA
RYIDAGASVLAKQSEDVMGMPFTDGFFKVIFSRDIPTLVEKNLKTNVQIFLDKHKLSF
HDISYFLAHPGGKKYIDAYIKSLGLSSEKLSSAGSILQKHGNNSSATILYVIKDHLQN
GHKKAAERGLIGALGGFSSELLLFSWEKGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /EC_number="2.3.1.74"
/note="25.6% of identity to the Lycopersicon esculentum
(tomato) naringenin-chalcone synthase; alternate gene name
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /translation="WTDQNKKELLHKTGELYKQFIENQDEQRAAKLAAVWKKAADEEV
YIAFTGHYSAGKSSLLNCLLMENILPTSPIPTSANLVVIRNGEKRVRLHTTDGACAEL
EGTYQKDKVQQYCKDGEQIESVEIFDRYTEIDSGVAYIDTPGIDSTDDAHFLSAASIL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /translation-"MAFILSIGTSLPAYNVNQEKAAEFARYMFQHSFKDIDRLLSSFK
NGQIHSRQFVKPIEWYKEGHSFEEKNQIYIEETLKHSRAAVRECLSHPEFFQEAIPYE
                                                                                                                                                                                                                                                                                                 VSIDIFMCGVATLLQVWSNRFFGIGLPVVLGCTFTAVSPMIAIGSEYGVSTVYGSIIA
SGILVILISFFFGKLVSFFPPVVTGSVVTIIGITLMPVAMNNMAGGEGSADFGDLSNL
                                                                                                                                                                                                                                                                                                                                                       ALAFTVLSIIVLLYRFTRGFIKSVSILIGILIGTFIAYFWGKVQFDNVSDAAVVQMIQ
PFYFGAPSFHAAPIITMSIVAIVSLVESTGVYFALGDLTNRRLTEIDLSKGYRAEGLA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 translation-"MFWLLIAILIVQRAAEMAVARQNEQKVKKQGAIEFGESHYPYII
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TMHILFFLSIIAEVILMNKOPSSWWIGIAAVILSVÕIVRYMALČSLGAVWNTKIIVVP
GVELVKKGPYKWMKHPNYAVVILEIILIPLLYQAYVTMCLFSIFNAVLLSVRIRAEDK
                   /function="pyrimidine salvage"
/note="26% of identity to the Bacillus caldolyticus uracil
transport prot. . .; putative"
                                                                                                                                                                                                                                                                          /translation-"MRNGFGKTLSLGIQHVLAMYAGAIVVPLIVGKAMGLTVEQLTYL
                                                                                                                                                                                                                                                                                                                                                                                                          VLLGGIFNAFPYTAFSQNVGLVQLTGIKKNAVIVVTGVILMAFGLFPKIAAFTTIIPS
AVLGGAMVAMFGMVIAYGIKMLSRIDFAKQENLLIVACSVGLGLGVTVVPDIFKQLPS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /note="33.3% of identity in 60 as with the Sacharomyces cerevisiae farnesyl cysteine carboxyl-methyltransferase;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /gene="ypbR"
5340. .8921
/gene="ypbR"
/note="26.7% of identity in 165 aa to a Thermophilic
bacterium hypothetical protein 6; putative"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                ALTLLTINGIVAGSFTAVVLNIVYNVFSKAKKIEQEADLAEQKTAV"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /product="naringenin-chalcone synthase"
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                                                                                                                                                                                     /product="transport protein"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /protein_id="AAA96614.1"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          3322. .3341
/note="putative"
/citation=[3]
3397. .4494
/gene="bcsA"
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                                                                                                                                                            /transl_table=11
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                                                                                                         /citation=[3]
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/gene="ypa0
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Losses 1 to 213680)

Kunst, F., Ogasawara, N., Yoshikawa, H. and Danchin, A.

Kunst, F., Ogasawara, N., Yoshikawa, H. and Danchin, A.

Submitted (18-NOV-1997) I. Moszer, A. Danchin, Institut Pasteur,

Regulation de l'Expression Genetique, 28 rue du Docteur Roux, 75724

Paris, Cedex 15, FRANCE. E-mail: moszer@pasteur.fr,

adanchin@pasteur.fr Phone: +33 (0)1 45 68 84 41, Fax: +33 (0)1 45
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KPGEFSPAKWQKRNEYMIDHSEAIVAVYDGSKSGTRNCLNYAKKTYLGHQLMRLHPDF
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CKACVLKKAKESMLKNYDKQLERMRERNLLPGMKEAKKKYNSSLKKKKTQQIWQEKNK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LKI.KNYRLQRDAHKKHNITDVQWQKCKDYFNNKCSYCGLKIEDHKILFKGTYIQSDFH
KEHVDHKGANDISNCIPACKSCNSSKHDFAFEEWYNSSNKNFSSERLLKIKEWLNFFK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /db_xref="SPTREMBL:034326"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /translation="MKNPTMLKLKDKLLAVIEELITKENKYRFITGGALGTDQAACWC
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Yoshida,K., Yoshikawa,H.F., Zumstein,E., Yoshikawa,H. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /note="similar to hypothetical proteins from B. subtills"
                                                                                         The complete genome sequence of the gram-positive bacterium
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1. .213680 //organism="Bacillus subtilis" /strain="168"
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                                                                                                                          Bacillus subtilis
Nature 390 (6657), 249-256 (1997)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /db_xref-"taxon:1423"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /gene="yoqL"
complement(90. .782)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /function="unknown"
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                                                                 Danchin, A
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AUTHORS
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                                                                                                                                                          JOURNAL
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                                                                                            TITLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Bacillus/Staphylococcus group; Bacillus group;
Bacillus/Staphylococcus group; Bacillus group;
Bacillus/Staphylococcus group; Bacillus group;
Runst,F., Ogaswara,N., Moszer,I., Albertini,A.M., Alloni,G., Azevedo,V., Bertero,M.G., Bessieres,P., Boldtin,A., Borchert,S., Bronillet,S., Bruschl,C.Y., Caldwell,B., Caphanno,V., Bornie,R.M., Denizot,F., Devine,R.M., Dusterhoft,A., Ehrlich,S.D., Emmerson,P.T., Entlan,K.D., Erritan,F.M., Connerton,I.F., Cummings,N.J. Daniel,R.A., Denizot,F., Devine,R.M., Dusterhoft,A., Ehrlich,S.D., Emmerson,P.T., Entlan,K.D., Erritan,F., Galser,P., Goffeau,A., Golightly,E.J., Galger,D., Fritz,C., Fujita,M., Fujita,Y., Fuma,S., Galizzi,A., Galleron,N., Ghim,S.Y., Glaser,P., Goffeau,A., Golightly,E.J., Harwood,C.R., Handt,A., Hilbert,H., Holsappel,S., Hosono,S., Hullo,M.F., Itaya,M., Jones,L., Joris,B., Karamata,D., Kasahara,Y., Kaerter,P., Khaerr-Blanchard,M., Kleip,C., Kobayashi,Y., Koetter,P., Knainois,S., Laubert,J., Lazarevic,V., Lee,S.M., Levine,A., Liu,H., Masuda,S., Mauel,C., Medique,C., Medina,N., Mellado,R.P., Lanbert,B., Makai,S., Prescott,A.M., Persecan,E., Purielle,D., Porwollik,S., Prescott,A.M., Persecan,E., Pulic,P., Ruvolta,C., Roche,E., Roche,B., Rose,M., Sadaie,Y., Sato,T., Senors,S.J., Serror,P., Shullon,B., Soldo,B., Soldo,B., Soldo,B., Soldo,B., Takahashi,H., Takamaru,T., Takahashi,H., Takamaru,T., Takahashi,H., Takahashi,H., Takahashi,H., Takahashi,H., Takahashi,H., Takahashi,H., Takahashi,H., Takahashi,H., Tamakoshi,A., Tanakoshi,A., Tanaka,T., Wedier,F., Takahashi,H., Takahashi,H., Takahashi,H., Takahashi,H., Takahashi,H., Takahashi,H., Takahashi,H., Takahashi,H., Wedier,F., Takahashi,H.,
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Bacillus subtilis complete genome (section 12 of 21): from 2195541
to 2409220.
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                                                                                                                                                       14273 TGC---GAAAACCTTGTCAAGGATGACCAAGTGCAAGTAGTTGTCGTGTGCGGGAAAAT 14217
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            14216 ACGCCTTTAAAAGAATCTTTGAGTGCGCTTGAAGCGGAAAATGGTGACAAATTAAAAGTT 14157
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    780
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ttcatagacgtaggtattgatccttcaacagttaaagtgacaggtattcctattgataac 543
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Best Local 9
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                    complement(2014. .2466)
                                                     complement(2014. .2466)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            73 agtatcgttaatcaacttaatgatatgaatctagaccatttaagcgtcattgagcacgat 132
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               aataaaaagatattgattattactggctcattcggtaacggtcatatgcaagttacacag 72
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Pred. No. 4.6e-12;
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Hesésanger.ac.uk or revenematode.wustl.edu

On Jun 20, 1998 this sequence version replaced gi:1888376.

IMPORTANT: This sequence IF unfinished and does not necessarily

IMPORTANT: This sequence IF unfinished and does not necessarily

represent the correct sequence. Work on the sequence is in progress
and the release of this data is based on the understanding that the
sequence may change as work continues. The sequence may be
contaminated with foreign sequence from E.coli, yeast, vector,
phage etc. Order of segments is not known; 800 n's separate
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                        Db 110996 CIGGCCTATGTGGAGCGCATTGATGAGCTATTTCGGATCACAGATTGCATGATTACCAAG 111055
                                                                                                        Db 111056 CCCGGCGCATTACTTTGACAGAAGCCACAGCCATTGGAGTGCCTGTCATTCTGTACAAA 111115
                                                                                                                                                                                                                                                                                                                                   Caenorhabditis elegans chromosome II clone Y53C12, *** SEQUENCING IN PROGRESS ***, in unordered pleces.
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                                                                                 cctggtggtatcacaataactgaaggtttcgcccgttgtattccaatgattttcctaaat 900
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NOTE: This is a 'working draft' sequence. This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.
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Rhabditoidea, Rhabditidae, Peloderinae, Caenorhabditis.
1 (bases 1 to 242893)
                                                                                                                                                                                     DD 111116 CCCGTGCCTGGCCAGGAAAAAGAAAATGCAAACTTCTTTGAAGA 111159
                                                                                                                                                                   cctgcacctggtcaagagcttgaaaatgccttttactttgaaga 944
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/organism="Caenorhabditis elegans"
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/chromosome="II"
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Caenorhabditis elegans.
Caenorhabditis elegans
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current sequence finishing criteria for the C. elegans genome sequencing consortium are that all bases are either sequenced consortium are that all bases are either sequenced unambiguously on both strands, or on a single strand with both a dye primer and dye terminator reaction, from distinct subclones. Exceptions are indicated by an explicit note.

IMPORTANT: This sequence is not the entire insert of clone Y53C12D. It may be shorter because we only sequence overlapping sections once, or longer because we arrange for a small overlap between
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Hinxton, Cambridge CB10 1RQ, England and Department of Genetics, Washington University, St. Louis, MO 63110, USA. E-mail: jesésanger.ac.uk or rwenematode.wustl.edu Coding sequences below are predicted from computer analysis, usin predictions from Genefinder (P. Green, U. Washington), and other
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              603 taagcaaactattttaatgtcagctggtgcatttggtgtatctaaaggttttgacacgat 662
303 aaaagaaaagccagatttaatattattaacgtttcctacaccagttatgtcggtactaac 362
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       543 caaatttgaaacgcctattaatcaaaagcagtggttaatagacaacaacttagatccaga 602
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                                                                                                                                                                                                                                                                     423 aaactggattacgccgtattcaacaagatattatgtggcaacaaaagaaacgaaacaaga
                                                                                                                                  363 tgagcaatttaacattaatattccagttgctacagtgatgacagactatcgcttacataa
                                                                                                                                                                                                                                                                                                                                                                                                     483 cttcatagacgtaggtattgatccttcaacagttaaagtgacaggtattcctattgataa
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Eukaryota, Metazoa; Nematoda; Chromadorea; Rhabditida;
Rhabditoidea; Rhabditidae; Peloderinae; Caenorhabditis.
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GI:3367637

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Ohta, H.
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neighbouring submissions.

He start of this sequence (1. .117) overlaps with the end of sequence 299277.

The end of this sequence (1390. .1496) overlaps with the start of sequence 299278.

Sequence 299278.

For a graphical representation of this sequence and its analysis see:- http://wormbase.sanger.ac.uk/perl/ace/elegans/seq/sequence?
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1324 AATAAATAAATATTAATTAAATAAATAATTTAATTAAATAAATAAATAAATAAATAATTAATT 1383
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                                                                                                                                                                                                                                                                                                                                                            agttacacagagtatcgttaatcaacttaatgatatgaatctagaccatttaagcgtcat 122
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Arabidopsis thaliana mRNA for monogalactosyldiacylglycerol
synthase.
AJ000331
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                                                                                                                   1. .1496
/organism="Caenorhabditis elegans"
/db_xref="taxon:6239"
/chromosome="II"
                                                                                                                                                                                                                                                                Mismatches 348;
                                                                                                                                                                                                                                    Score 60.2; DB 6;
Pred. No. 0.15;
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/LTAINSTALTON-**MATTYWALARKVLERVYGTSKSAVSVTSGDGEKTHRHTHHHIHR
IKSYDDIDEDESSLELIOLGAERTRNYLILMSDTGGGHRASARAIRDAFKIEFGDKYR
YTKDVWKEYTGWPLNUMERSYKFWYKHVYWYRYSTSPKWHIHSCYLAAIAAYAK
EVERGILMEYKPEIII SVYPLMAHIPLWYLKYGELOKRYLFYWYIDINYCHPTWFHPG
VNRCYCPSQEVAKRALFDGLDESQVRVFGLPVRPSFARAVLVKDDLRKELEMDQDLRA
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VKYREFEDQMEKWMGACDITTKAGPGTIAESLIRSLDIILNDYIPGQEKGNVPYVVE
NGGVYFTRSPKETARIVGEWFSTKTDELEQTSDNARKLAQPEAVFDIVKDIDELSEQR
GPLASVSYNITSSFALLV
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                                 Arabidopsis thaliana
Eukaryota; Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta;
Magnodlophyta; eudicotyledons; core eudicots; Rosidae; eurosids II;
Brassicales; Brassicaceae; Arabidopsis.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Direct Submission
Submitted (08-JUL-1997) Ohta H., Faculty of Bioscience and
Biotechnology, Tokyo Institute of Technology, 4259 Nagatsuta
Midori-ku Yokohama, Kanagawa/226, JAPAN
Revised by [3]
2 (bases 1 to 1648)
                                                                                                                                                                                                                                                                                                                                       Awai,K., Shimojima,M., Masuda,T., Takamiya,K.I. and Ohta,H. CDNA cloning of an Arabidopsis monogalactosyldiacylglycerol synthase revealed that the enzyme belongs to an uridine diphosphate-utilizing glycosyltransferase superfamily
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/product="monogalactosyldiacylglycerol synthase"
/protein_id="Cad04005.1"
/db_xref="01:336/638"
/db_xref="01:336/638"
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mgd gene; monogalactosyldiacylglycerol synthase.
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Submitted (13-OCT-1998) Department of Genetics, Washington
University, 4444 Forest Park Avenue, St. Louis, Missouri 63108, USA
4 (bases 1 to 44352)
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Submitted by:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida;
Rhabditoidea; Rhabditidae; Peloderinae; Caenorhabditis.
1 (bases 1 to 4435)
The C. elegans Genome Sequencing Consortium, Washington University
Genome Sequencing Center, St. Louis U.S.A. and the Sanger Centre,
Hinxton, U.K.,C.
Genome sequence of the nematode C. elegans: a platform for
Investigating biology. The C. elegans Sequencing Consortium
Science 282 (5396), 2012-2018 (1998)
941
                                                                                                                                                                                                                                                                                                                                                     24-SEP-1999
                                                                                                                               882 tecaatgatttteetaaateetgeaeetggteaagagettgaaaatgeettttaetttga
                                                         822 tcaacttatgattacgaaacctggtggtatcacaataactgaaggtttcgcccgttgtat
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2 (bases 1 to 44352)
Wamsley,P. and Gibson,A.
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Unpublished (1999)
3 (bases 1 to 44352)
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Caenorhabditis elegans cosmid H28G03.
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Coding NOTES: gene gene CDS FEATURES Department of Genetics, Washington University, St. Louis, MO 63110, USA, and Sanger Centre, Hinxton Hall Cambridge CBlO IRQ, England e-mail: rw@nematode.wustl.edu and jes@sanger.ac.uk

## NEIGHBORING COSMID INFORMATION:

ďq The 5' clone is T03G11, 4800 bp overlap;3' clone is Y34B4A, 6600 overlap. Actual start of this clone is at base position 78 of CELH28G03; actual end is at 37952 of CELH28G03

ygue-/protein\_id="AAC67404.1" /db\_xref="GI:3786418" /translation="MQRDNVIDSAGNPPVENPDIDLQDGEIGEESFEATQAYLQDMEN SAEA I ALERQRAEEA MATMDEDDOGINEFGRRRNPPRTPPPBRAPEGOPTCESIGFYN EBFDDVSDDGEI PGRKRIGPKTPPPEBPESPKOI EQTREGGSDGELTGDDMEPI PIIEP KLNKESKREKRHATREVHSRKRRHDDKKRSTVRPEVSKELTFPVVATQKCLSLLEFVE KRGLTITDDELLQVVRDSIELDQAMGKIVKKKRAMKKOMEDMAMELEKIKRIHANMP RHMQDVLKTOGKTVHIAQERPMPPMPFSASSIVSLKYGQPMPHHMGMPPPGMGPPPF MPPPIGMPPPLGMPPPHIGGAAPTAYPPPMSLLGPPPFSVPPSYSPAAPIV PPPPVOSTAQPPPSGTSEAEKMWTHGLNPIAFSNAPPGLKCGMNDYNQPPPAKKPAA QONPQMNRITNNLSSMLTNALKAQVSKAQNSLNNSSPTSTAPKKPVPSLMSINIPGVP Coding sequences below are predicted from computer analysis, using the program Genefinder(P. Green and L. Hillier, ms in preparation). Location/Qualifiers join(6742. .7098,7438. .7536,7588. .7643,12371. .12518, 15241. .15466,15654. .15705,15761. .16121,16167. .16298 /organism="Caenorhabditis elegans" /gene="H28G03.2" /note="coded for by C. /db\_xref-"taxon:6239" /strain="Bristol N2 6742. .16476 /gene="H28G03.2" /chromosome="X" /clone="H28G03' .16476) 1. .44352

17763. .18923 /gene="H28G03.1" KAGSSGSQN"

join(17763, 18017,18067, .18228,18281, .18781,18831, .18923) /gene="#28G03.1" /note="Contains similarity to Pfam domain: PF00076 (rrm), Score=105.1, E-value-4.4e-28, N-2.; coded for by C. elegans CDNA yk171a8.5; coded for by C. elegans cDNA yk171a8.5; coded for by C. elegans cDNA yk171a8.3;

/codon\_start=1

/protein\_id="AAC67401.1" /db\_xref="G1:3786415"

ETDPAPGCKLLLNGITNGVHSVDSLRVYFETFGTLDQVEILGQPRGLGFVIYEDKESA DRCLAHNSGRHIVNERKIEVRFTKHPNGSTYWKRPQSQSHSQRDLFEQLSQLNLKDG DRKSTGNSSSAADTPQNFDEDSNYGGTTTEDDCNVFEHEEGSSEESSTEQTLENEKEN FKYALFQQFQQMGMGQYQHDSPPQLRKLFIGGLSHDTTDEQLGNYFSQWGPVVDAIVI RDPNTKHSRGFGFVTFASIFSAESAMNDRPHKLGGKTVDSKRAIPREQMSSMIPPPFF /translation="MNHECLILRRMHISDLITILELPYLWDTFKVSKKNNLKLGVRSI

This sequence was finished as follows unless otherwise noted: all regions were double stranded, sequenced with an alternate chemistry or covered by high quality data (i.e., phred quality >= 30); an attempt was made to resolve all sequencing problems, such as compressions and repeats; all regions were covered by sequence from more than one m13 subclone.

NOTICE: This sequence may not be the entire insert of this clone. It may be shorter because we only sequence overlapping sections once, or longer because we provide a small overlap between

neighboring submissions.

complement(21324, .22960)

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CDS

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Current sequence finishing criteria for the C. elegans genome sequencing consortium are that all bases are either sequenced numbiguously on both strands, or on a single strand with both a dye primer and dye terminator reaction, from distinct subclones. Exceptions are indicated by an explicit note.
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                                                                                                                                                                                          176 aatggtatatcaatagctttaaatattttagaaatatgtacaaagggttttattacagcc 235
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                                                                                                                              56 atatgcaagttacacagagtatcgttaatcaacttaatgatatgaatctagaccatttaa
                                                                                                                                                                                                                                                             116 gcgtcattgagcacgatttatttatggaagctcatccaattttgacttctatttgtaaaa
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        356 tactaactgagcaatttaacattaatattccagttgctacagtgatgacagactatcgct
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Erratum: [[published errata appear in Science 1999 Jan 1283(5398):35 and 1999 Mar 26;283(5410):2103 and 1999 Sep 3;285(5433):1493]]

(bases 1 to 152878)
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Ceanornabolitis elegans cosmid Y18D10A, complete sequence.
AL034393 AL0108871
AL034393.1 GI:3979928
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Rhabditoidea; Rhabditidae; Peloderinae; Caenorhabditis.
1 (bases 1 to 152878)
   Length 44352;
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      DB 6;
   Score 56.8; DB Pred. No. 0.43;
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/db_xref-"G1:5921682"

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/db_xref-"G1:5921682"

/dranslation-"MRDPDKVKSGPICDTVAVIVLEESDDENALPDVLHEVQSPHTSD

/translation-"MRDPDKVKSGPICDTVAVIVLEESDDENALPDVLHEVQSPHTSD

NIPTESIKKERPRGMYNGSVESPEEFYQILTTERGTRRAYLSTWEEDERTLINFK

AVSTVIJSOMFHPRARETHLEISNDLATPERSSSELIRFITYELVEBGSTIEIRTK

TLHVELGEFELIPISVTGKDVAMLFKMLGFQNVIXIIHALLSDCRITVLASSSLMRLSR

CQNAILSLLYFFEYHBGCYTILDSLABVLESPTFFLGVLSEFYGFGCBNIYVYLD

NGFHYPDRALIT KSDDYYTILDSLABVLESPTFFLGVLSTPRERE TEVDDFILLOKK

LRACFITYRFALLYGYQYTILTRT KIGNFRKLITTSLTFHVGARFREKTTDMMSSSL

LKSYYFQTFILTRAALPRRHDLEDELSGFKELDQLIFKQNSTSSESKK IT EHISGELI

QKERYMEKCSARROBIFTK HHUISGRELAQNNNSI IHTVFRKRSNVILOAMLPVVNT

HAEYHANQFENTARLELLANGLAAFFGKVAPSKSLADVKSSMRFALLETELECRLL

NQKCSHDKLITDRQFEDIALLANDAALQAECEEDKDGVVRSLMYLSNVYSSRKVAGGWQY

MYTAVOGHKVWRNQRFWTSCFYYEVHEMLFSEMLQKDRKITESLWCHTLRPCAMEMIN
                                                                                                                                                                                                                                                                                                                                       /translation="MLHHQAQRENLKIENLKTMIPLHVHHLHYTVKLIFTEKSPHSPT
YNPDSPSYGEPSVAAEQQRPASSARYNVGPANNFAVQTPSPAQIAAMGYSGVSTVEYE
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ITYMIPQIIMPLQHIFHESNNMSQKFKFSQNHLIITIFF".

complement (23377 . 25416)
/gene="H28G03.4"
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RFKELGNFSDRSGRGKPPTAYKKSTCQFLSEAAKIKRKDRAMNLLRRFRNGAHRKVLF
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TKWRNNYYLDMKTPELMPWKKHFKKTKWTPQQDGAPAHKHKNVQAMCBSNFPDF TAF
NQWPPSSPLLNPMDYSWWSVLEARACSKPHRNI DSLKDSLKKAMDELD I NYLRATVDS
FPRRLEASRELLT I LITHPVWSK WWISLE I PYLRATVOBFPKRYRYCL FRADGDI FELM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /translation="MNTSHHVSDEPVKLFKTSTSKNHILDEPFIIRLHLIDPSIHHIH
                          complement(join(21324. .21442,21532. .21738,21823. .21870,
22258. .22314,22364. .22439,22516. .22554,22598. .22636,
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FLISDPIDCYLLTSIEESEMSLNRLENLLPADGSLFLTNYRVIFKGKSVDINATNGTI
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AIEKFLEVIETNSHNSFAFYNTRKDMKVVENGSHKFGTLNSAIRGFTKKKTDTRRIRS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              complement(join(23327. .23464,23548. .23591,23709. .24369,
24510. .24685,24923. .25036,25170. .25416))
/gene="H28G03.4"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          HSSHRGSIQLSFDKMEELDYLKKNAHIRYAVIDYPRIGLNSKIVKLRMSHSNLDYTIC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /note="Contains similarity to Pfam domain: PF00292 (PAX), Score=10.2, E-value=0.028, N=1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 complement(join(35875. 35970,36016. 36302,36349. 36498
37005. 37060,37112. 37340,37388. 37724,37774. 38040,
38522. 38760,38806. 38926,38970. 39421,39473. 39782,
40206. 40306,40368. 40926,40975. 41121,41199. 42050,
42271. 42471,42529. 42622,42673. 42805,42990. 43284,
43778. 43968,44229. 44307))
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /_note="contains similarity to Pfam domain PF00169 (PH), Score=19.5, B-value=4e-05, N=1; coded for by C. elegans CDNA yk53a7.3; coded for by C. elegans cDNA yk47d2.3; coded for by C. elegans cDNA yk126b8.3; coded for by C. elegans cDNA yk126b8.3; coded for by C. elegans cDNA yk194d7.3; coded for by C. elegans cDNA yk194d7.3; coded for by C. elegans cDNA yk194d7.3; coded for by C. elegans cDNA yk194d7.5; coded for by C. elegans cDNA yk194d7.5; coded for by C. elegans cDNA yk12tc6.3"
                                                                                                                                                      /note="contains similarity to intermediate filament
proteins (Pfam: filament.hmm, score: 15.43)"
                                                                                                                                                                                                                                                      /evidence=not_experimental
/protein_id="AAC67402.1"
/db_xref="GI:3786416"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /evidence=not_experimental
/protein_id="AAC67403.1"
/db_xref="G1:3786417"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  complement(35875. .44307)
/gene="H28G03.6"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /codon_start=1
                                                                                                                                                                                                                            /codon_start=1
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CDNA
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                                                                                                                                          The
                                                                                                                                                                          The start
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KKRSKGTGETVGDVIKKRLROTAKTTATVIHTPOPDILATKKRERMRAPATATVSKKE
KRKNAGSADSSIVEEHEDETMILLEGOTLDILPOQTSQOEPRISGSELLDEQPBASEE
HGGTVPSAPELIKNPAPPVPEASEASAEPPKIDIPEQATPILALALALPTVSPTALEP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    VTTLKAAKIENSSKTKKLDKYLKSVIQVVDALSSTSNLSKQSKSIKDLVTVFRRDDVR
LFFNSQPWKNSLSTSDPSISATEAEASEDPEHLDDVITEPAPPIGEQTLSDDEEEEEE
VPEDEADDEVDREIRQLENELLQRVKEKTVRRPDFTAKMIELKAKSRAPRLVETKFVK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PKAQENPTAELPTTSEISGRAPQALPTSSQTPPTSGSAAPPVDDLLSEILSGAKTTKT
RKAAPPAVQKSISSTTQQAPPTSVQAPPTSCSAAPPVDDLLSEILSGAKTTKTTKTTK
MPPVDQKKISSEAPPISDSAPTSVHQQTPKSPKQILNSKYGLDISDSEDEEEEERG
IMPORTANT: This sequence is not the entire insert of clone Y18D10A. If may be shorter because we only sequence overlapping sections once, or longer because we arrange for a small overlap between neighbouring submissions.

The true left end of clone F0BAB is at 152766 in this sequence. The true right end of clone B0019 is at 105 in this sequence. The crue right end of clone B0019 is at 105 in this sequence. The start of this sequence (1..105) overlaps with the end of sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /db_xref="SPTREMBL:09XW25"
/translation="MDEDIAEAQCASEGCANVRKNLGLLLMQNKQRAAEMQDFSKVQA
ECEVLRMKLVSTDAAYRESVQREAEAINAKEIAEASLKQGQYDSEFYKKKSASLQEQA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        KWPEGIHKPTEKDSFGLLNSTKIHRNOFPTSDFETIAQATAERKKALLGAQGAAGASE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PGSSSSIHGKKGKTVRELQTEMMKGESVKEKAARMRAEASAGRSQAPGPAPAAASEL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           QDPPQDFGLSMSDPGSDSETEEHQKQEKHIPAMVTRRSARLSALPVTPKKASSSSKMP
PPPSPSPSTPGRRGRRPRTLSTMSMEPAAAAVTPAPRGRPRSRSAAKVSENTEPLSEA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         VLPPSSSSSTEPPSAPDSASTTSSMKKGGGAIMIEAVPCRPGGKAIKREQKPIGMKEM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MVQNVEKGGKKVNKIKTHLRQALDLKIPFEELKRPMEEKGIKLGDSIPLTPSDAVDVM
MEFLRETSAADMWAVLNRQRIDANLKPLMNKEEENFLQVSVTLNEHDQQLLEVFISRI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NVAFDFLRQKMDLIEEQFLKPKEMEKEPKRITAFSVPTVVTKMTKSEAEMLKKESKWQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DDAEKHKDQANYWRNKYDSVCALTERLEANNIDIKSKYESTVKLLETAGKRMTSLDNQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEIVEEEEEAPPISDSLQASEPSSTATVKPEKVVAVVKIFSPEIDSTSVEAPPEASVP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PKAPAATKIDNQLADQQASEPEPPKARKLPIARKIPPKIKISLPAPSSSTTSDDDLMS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DILAGAKTTKTTKPKAPPTRVAQTTRTKNLAQKRKASPPTPAGTTAPKRQYIKKSIDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             IFELCARESIGSNECGRLIRLFCHAVRFSESAENPDDVTSPVYQKKSTWIRRLFQILL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LNHPNQIGKSTCYILMSDVAKYCRFLVVEEMDKDHMGSEFHLAFRVLMHKDSEQASAV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NWLLNAKFDVAYVAPPTSNDVTEACINAHKQCIDDDDVTPSLLKKSIFLAKTAAPEVL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    KNVLRVMIDNPFSSHSHAIFAALKQISPQVSQLREIIESSEINQYVEMTGEDAIRDAV
                                                                                                                                                                                                                                                               The end of this sequence (152766. .152878) overlaps with the start of sequence 299710.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             .9924,10879. .11164,
.16655,17748. .18104,
.20807,22205. .23127,
.26130,26236. .26256))
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          complement(join(7920. 8081,9752. 9924,10879. 11164,
12359. 12699,13906. 14204,15129. 16655,17748. 18104,
19860. 19949,20008. 200088. 20089. 20807,22205. 23127,
24486. 24744,25724. 25909,26020. 26130,26236. 26256))
                                                                                                                                                                                                                                                                                                                                   For a graphical representation of this sequence and its analysis see: http://wormbase.sanger.ac.uk/perl/ace/elegans/seq/sequence?
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   .27405,27490.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    cDNA EST yk54lb5.5 comes from this gene"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              27624 . .27788,28732 . .29006))
/gene="X18bloA.2"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   26573,27346.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      complement(join(7920. 8081,9752. 12369. 15599,13906. 14204,15129. 19660. 19949,20008. 20088,20709. 24486. 24744,25724. 25909,26020. /gene="Y18D10A.1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /organism="Caenorhabditis elegans"
/db_xref="taxon:6239"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        'note="predicted using Genefinder
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                .27788,28732. .29006))
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ONLVDLISIYTNFPLKPTTLPPSS"
complement(join(26502. .2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /protein_id="CAA22308.1"
/db_xref="GI:3979929"
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                                                                                                                                                                                                                                                                                                                                                                                                                                      Location/Qualifiers
1. .152878
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /gene="Y18D10A.1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /gene="Y18D10A.2"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /clone="Y18D10A"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /chromosome="I
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /codon_start=1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /codon_start=1
                                                                                                                                                                                                                                                                                                                                                                                                      name=Y18D10A
                                                                                                                                                                                                                            AL008866.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          source
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CDS

CDS

FEATURES

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/translation="MTGERQTEAVSKRSNVVSERCGGPPCLRLVDGRTLSVCVSDDSS HIDGSTGYRPESDCLSLSTLTSTAAVPATASSSSERAFGVSSTELWARTS VSULLVARVVSULLVARVSTLAGGARDATASSSSERAFGVSSTELWARTS VSULLVARVV VGVLLVTGGWREKTIVWOPFHRLPTRKRENSFRSSFFCFLKPMIGGWTLSF" join (39072. 39164,40245. 40513,41360. 41936,44226. 44375) /gene="Y18D10A.5" /0046="Y18D10A.5" /0046="Y18D10A.5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Join(47525. .47593,48112. .48208,48610. .48751,49616. .50045,
50501. .50818.51553. .51971,52106. .52364,52847. .53224)
/gene="X18D10A.6"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       .50045,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TAAHYPKSNVAVLCGPGNNGGDGFVCARHLOOFGFPPSIVYRKESRNBLMKSLVVOCE
TSSIPITATLPTNLOAFPLIVDALFGFSFHPPTREPFTEMLKTVRASGIHVFSIDVPS
GWDVELGAPSGNDDDVIHPHSVISLTLPKLCMKNWTGPHFLGGRFVPKSLVDEHELLM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /translation="MDGSGEKAIGFLIQFSLNARFWTDKQLLATDEPFSSENYQWYRR
FRIISEKRPKSVDKLYKTGEIPARGRGNKVGGRVFSKMPISKSMELSLVKLKQTPIIQ
QFYMKNGKKSTWVHIISKKTVSFIGQKLAAQIDEQLFTKYGFKVEQLMELAGLAAAQA
                                                                                                                                                                                                        SRCPDTSKFIHNQLVPFYQNYKGNLSDGLKLDFHAVPTGGHQVDGKYVNRCLHGALEC
                                                                                                                                                                                                                                                               ALNKLQMCSKKHIKQDWLVTAGCIQGKTAYSAGLKCLPDTEEGKIVQNCAESEEGEYL
LNDENSYRYNVAPHSAWLPWIQVNGERNRNAEFKLKDFSSVFRLFFEVFLQKCLKRSI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /translation="mnkQLLSCSLKSGKQVTMVVASVATDGVDQOVEISYYDQKVIGN
GSFGVVFLAKLSTTNEMVAIKKVLQDKRFKNRELQIMRKLNHPNIVKLKYFFYSSGEK
KDELYLNLILEYVPETVYRVARHYSKQRQQIPMIYVKLYMYQLLRSLAYIHSIGICHR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DIKPQNLLIDPESGVLKLCDFGSAKYLVRNEPNYSYICSRYYRAPELIFGATNYTNSI
DVWSAGTVMAELLLGQPIFPGDSGVDQLVEIIKVLGTPTREQIQSMNPNYKEFKFPQI
KAHPWNKVFRVHTPAEAIDLISKIIEYTPTSRPTPQAACQHAFFDELRNPDARLPSGR
                                                                                                                                          /translation="MQMNPNKSPPISINFPLFTMSKFLLFISISAVATASDLVEVFG]
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           .31522,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                join(47525. .47593,48112. .48208,48610. .48751,49616. .56
50501. .50818,51553. .51971,52106. .52364,52847. .53224)
/gene="Y18D10A.6"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       complement(join(29879, .30346,31220, .31296,31346.
34557, .34852,35323, .35351))
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Submitted (07-SEP-1999) Nematode Sequencing Project, Sanger Centre, Hinxton, Cambridge CB10 1R0, UK and Department of Genetics, Washington University, St. Louis, WO 63110, USA. E-mail: hes@sanger.ac.uk or rwenematode.wustl.edu on Nov 21, 1998 this sequence version replaced g1:3873430. IMPORTMANT: This sequence version replaced g1:3873430. IMPORTMANT: This sequence is unfinished and does not necessarily represent the correct sequence. Work on the sequence is in progress and the release of this data is based on the understanding that the contaminated with foreign sequence from E.coli, yeast, vector, or the sequence may be contaminated with foreign sequence from E.coli, yeast, vector,

Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea; Rhabditidae; Peloderinae; Caenorhabditis. 1 (bases 1 to 247332) Harris, B.

Direct Submission

TITLE JOURNAL

COMMENT

AUTHORS REFERENCE

Caenorhabditis elegans. Caenorhabditis elegans

SOURCE ORGANISM

KEYWORDS

phage etc. Order of segments is not known; 800 n's separate

NOTE: This is a 'working draft' sequence. This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.

/organism="Caenorhabditis elegans

Location/Qualifiers

source

FEATURES

/db\_xref="taxon:6239" /chromosome="1"

/clone="Y18D10"

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MFFFSACLGVGIGLL&ALLFKHVDLRKTPSLEFALLLIFSYIPYGFAEALDLSGIMAI
                                                                                                                                                                                                                                                                                                                                           FWSVVLCLLGRACNVFPLAYLVNQCRKDVQISMKNQIIMWFSGMRGAVCFALVLYMDL
DKEKKSILLTTVLFLILFTTIFLGGSALPFISFINRCYPNERQRKRRRTPRNKESTGN
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                                                                                                                                                                      /translation="MMLSVEEQVLRNNIELMFTFNSLKILANGVTWQLWESTLNQGTA
                                                                                                                                                                                           TSGIMRFALKTALSICIFLLIFQTVDSDSSDSSASASVVSGAVKSEDTVVAVNKTDVL
GEAIDANATSLEQHGAAIVGNVSEEKKRSLAIFFILFVIMLATLVVHMLIVSKIHWMP
                                                                                                                                                                                                                                      ESLAIVALGALIGSILSYSRRDWSEIEALSPDVFFLVLLPPIIFENAYNLNKGYFFSN
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ALTKRALASDQMTDSDDVEFGGGGGGGGGRWKDDVTPTRGRSGSRNSSDVIISAGGG
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(Sodium/hydrogen exchanger family), Score=354.0, E-value=5.3e-103, N=1"
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\*\*\* SEQUENCING IN

Caenorhabditis elegans chromosome I clone Y18D10, PROGRESS \*\*\*, in unordered pieces.

247332 bp

CEY18D10

DEFINITION

ACCESSION VERSION

RESULT 15

CEY18D10 LOCUS

AL008871.1 GI:3900862

07-SEP-1999

us-09-668-788-3.rge

Oy 735 gogttctttaacagctaagtttaaattaacgaga 768
Db 77817 TAAATATTAATTAAATAAATAATTAAA 77850

Search completed: June 29, 2001, 12:01:42 Job time: 8915 sec

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n 4.5 Compugen Ltd. Compugen Ltd. Search time 162.85 Seconds (without alignments) 3759.313 Million cell updates/secgtaaaacgctgatactccag 975 idues meters: 1460202	segn/NA1980. DAT: * segn/NA1981. DAT: * segn/NA1981. DAT: * segn/NA1982. DAT: * segn/NA1983. DAT: * segn/NA1986. DAT: * segn/NA1986. DAT: * segn/NA1989. DAT: * segn/NA1989. DAT: * segn/NA1989. DAT: * segn/NA1999. DAT: *	cted by chance to have a score distribution.  Description staphylococcus aur MurE gene. Staphy Oligonucleotide Dl
GenCore version 4 Copyright (c) 1993 - 2000 c Sleic search, using sw model June 29, 2001, 11:49:30; Sea US-09-668-788-3 1 atggttactcaaaataaaaa IDENTITY_NUC Gapop 10.0, Gapext 1.0 730101 seqs, 313950809 residu	length: 0 length: 200000000 length: 2000000000 Maximum Match 0% Listing first 45 summe N_Geneseq_0601:* 1: SIDS8/gcgdata/gene 3: SIDS8/gcgdata/gene 4: SIDS8/gcgdata/gene 5: SIDS8/gcgdata/gene 6: SIDS8/gcgdata/gene 7: SIDS8/gcgdata/gene 7: SIDS8/gcgdata/gene 8: SIDS8/gcgdata/gene 9: SIDS8/gcgdata/gene 10: SIDS8/gcgdata/gene 11: SIDS8/gcgdata/gene 12: SIDS8/gcgdata/gene 13: SIDS8/gcgdata/gene 14: SIDS8/gcgdata/gene 15: SIDS8/gcgdata/gene 16: SIDS8/gcgdata/gene 17: SIDS8/gcgdata/gene 21: SIDS8/gcgdata/gene 21: SIDS8/gcgdata/gene 21: SIDS8/gcgdata/gene 21: SIDS8/gcgdata/gene	ન보면 OΣ!
OM nucleic - nuc Run on: Title: Perfect score: Sequence: Scoring table: Searched: Total number of	Minimum DB seq Maximum DB seq Post-processing	Pred. No. score gree and 1s der and 1s der No. Score (1 883.2 c 2 182.2 c 4 182.2 c 6 182.2 c 7 182.2 c 6 182.2 c 7 182.2 c 7 182.2 c 9 175.2 l 11 175.2

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This sequence represents one of 5191 Staphylococcus aureus DNA sequences of the invention. The DNA sequences are recorded on a computer readable medium, preferably selected from a floppy or hard disk, random access meaning. (RAM), read-only memory (ROM) or CD-ROM Homology searches using the S.aureus DNA sequences allows putative functions to be assigned so that protein-encoding or regulatory regions of commercial, therapeutic or industrial importance can be obtained. Specifically, sequences which are ILKely to encode antigens have been identified and these polypeptides can be used in a vaccine composition against S.aureus infection. The collypeptides can also be used in a kit for the immunodetection of S.aureus in a sample. S.aureus is implicated in numerous human diseases, including cellulitis, eyelid infections, food poisoning, osteomyelitis, skin and surgical wound infections, scalded skin sydarome, toxic shock contained the composition are useful as primers or probes for isolating committer readable mackin...
                                                                                                                                                                                                                                                                                                                                                                              these bases represent a line of missing text in the sequence listing in the specification. They are included to maintain the nucleotide numbering given in the specification for this DNA sequence"
are included to maintain the nucleotide numbering given in the specification for this DNA sequence".5640
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                                                                                                                                given in the specification for this DNA
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                                      ctaggttataccaaacacatgaatgaatggatggcatcaagtcaacttatgattacgaaa
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90.6%; ilarity 92.4%; Conservative

Local Similarity nes 902; Conserv

Best Loca Matches

Query Match

DB 18; Length 12658;

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CAAGTTACACAGAGTATCGTTAATCAACTTAATGATATGAATCTAGACCATTTAAGCGTC 438
                                                                  121 attgagcacgatttatttatggaagctcatccaattttgacttctatttgtaaaaaatgg
                                                                                                                                                                                                                                                                                                                                                                                                                    Electron-transfer group; ETM; mismatch; genotyping;
                                                                                                                                                                                                                                                                                                                             AAF58252 standard; DNA; 936
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                                                                                                                                                                              /product= "UDP-N-acetylmuramoyl-L-alanyl-D-glutamate:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Staphylococcus aureus can cause both invasive and toxigenic Infections which lead to diseases such as osteomyelitis, septic arthritis, septic thrombophlebits, such as steemyelitis, septic thrombophlebits, such as antibodies may be to treat individuals with these diseases and as a prophylactic to treat individuals with these diseases and as a prophylactic angainst them by bathing wounds and coating implanted devices. Antagonists of MurE may also be used to treat diseases caused by Heliobacter pylori infection such as stomach ulcers and gastrointestinal carcinoma. This method of treatment of bacterial infection is advantageous since many strains of Staphylococcus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    aureus are now resistant to some or all of the standard antibiotics. MurE is an important enzyme in bacterial metabolism and so the identification of such an enzyme in Staphylococcus aureus can be used to effectively diagnose and treat diseases caused by this
                                                                                                                                                                                                                                                                                                                                                                                                          Staphylococcus aureus useful for diagnosing and diseases such as osteomyelitis and toxic shock
                                                                    MurE; Staphylococcus aureus; infettion; treatment; diagnosis; primer; osteomyelitis; septic arthritis; septic thrombophlebitis; PCR; scalded skin syndrome; antibody; antibiotic; ds.
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           AAX08512;
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BP

(first entry)

437

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Nucleic acids containing electron-transfer group, useful as labels in hybridization assays, e.g. for genotyping, allowing repeat analyses on
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                                                                                                                                                                                                                                                                                                                                                                 (CLIN-) CLINICAL MICRO SENSORS INC.
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ETM; mismatch; genotyping;
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                                                                 Electron-transfer group;
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       AAF58254 standard; DNA;
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                                                                                                      WO200107665-A2.
                                     24-APR-2001
                                                                                       Synthetic.
                      AAF58254;
AAF58254/c
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Nucleic acids containing electron-transfer group, useful as labels in hybridization assays, e.g. for genotyping, allowing repeat analyses on
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Conservative 532; Mismatches 240;
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                The present invention relates to a composition comprising two nucleic acids each containing an electron-transfer group (ETM) having different redox potentials. The invention is used for electronic detection of nucleic acids, especially of substitutions (mismatches)
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ID AAF58257 standard; DNA; 936
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17-MAR-2000; 2000US-0190259
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ID AAF58259 standard; DNA; 936
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           group, useful as labels in allowing repeat analyses on
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                                                                                                 acids each containing an electron-transfer group (ETM) having different redox potentials. The invention is used for electronic detection of nucleic acids, especially of substitutions (mismatches) and single-nucleotide polymorphisms, e.g. for genotyping,
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                                                                                                                                                                                                                 Length
                                                                                     relates to a composition comprising
                                                                                                                                                                                                                                        Indels
                                                                                                                                                                                                                  22;
                                                                                                                                                                                                               Score 182.2; DB 22;
Pred. No. 4.8e-31;
32; Mismatches 240;
                                                                                                                                                                          Sequence 936 BP; 6 A; 138 C; 8 G; 8 T; 776 other;
                                                                                                                                                                                                                                       Conservative 532; Mismatches
           acids containing electron-transfer
                        assays, e.g. for genotyping,
                                                           Example 6; Page 128; 159pp; English
                                                                                                                                                                                                               18.7%;
0.9%; F
                                                                                                                                                    monitoring gene expression.
                                                                                     present invention
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group, useful as labels in allowing repeat analyses on
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Pred. No. 4.8e-31;
2; Mismatches 240; Indels
                                                                                                                  Electron-transfer group; ETM; mismatch; genotyping;
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Best Local Similarity 0.9%;
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              AAF58262 standard; DNA;
                                                                                         Oligonucleotide D2007
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group, useful as labels in allowing repeat analyses on
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agcaatttaacattaatattccagttgctacagtgatgacagactatcgcttacataaaa
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18.7%; Score 182.2; DB 22;
llarity 0.9%; Pred. No. 4.8e-31;
Conservative 532; Mismatches 240;
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                                                                                                                                                                                                                                                                                                                       Indels
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                                                                                                                                                                                                                                                                           Sequence 936 BP; 4 A; 139 C; 10 G; 7 T; 776 other;
                                                                                                                                                                                                                                                                                                             Similarity 0.4%; Pred. No. 1.6e-29; 3; Conservative 532; Mismatches 245;
                                                                                                                                                                                                                                                                                                      18.0%; Score 175.2;
                                                                                                                                                                                              Example 6; Page 127; 159pp; English
                                                                                                       (CLIN-) CLINICAL MICRO SENSORS INC
                                                           26-JUL-2000; 2000WO-US20476.
                                                                            26-JUL-1999; 99US-0145695
17-MAR-2000; 2000US-0190259
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Best Local Similarity
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Nucleic acids containing electron-transfer group, useful as labels in hybridization assays, e.g. for genotyping, allowing repeat analyses on
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                                                   aagagctaaaagcgttctttaacagctaagtttaaattaacgagaatgtatttgattctag
545 aatttgaaacgcctattaatcaaaagcagtggttaatagacaacaacttagatccagata
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Electron-transfer group; ETM; mismatch; genotyping;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DB 22;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Example 6; Page 127; 159pp; English.
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0.4%; F
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17-MAR-2000; 2000US-0190259
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Nucleic acids containing electron-transfer group, useful as labels in hybridization assays, e.g. for genotyping, allowing repeat analyses on a single surface

WPI; 2001-159728/16

Umek RM;

Example 6; Page 127; 159pp; English

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17-MAR-2000; 2000US-0190259
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The present invention relates to a composition comprising two nucleic acids each containing an electron-transfer group (ETM) having different redox potentials. The invention is used for electronic detection of nucleic acids, especially of substitutions (mismatches) and single-incleotide polymorphisms, e.g. for genotyping, monitoring gene expression.
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.larity 0.4%; Pred. No. 1.6e-
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ilarity 0.4%; Pred. No. 1.6e-29;
Conservative 532; Mismatches 245;
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                                                            BP.
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                                                           AAF58259 standard; DNA; 936
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Nucleic acids containing electron-transfer group, useful as labels in hybridization assays, e.g. for genotyping, allowing repeat analyses on
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Nucleic acids containing electron-transfer group, useful as labels in hybridization assays, e.g. for genotyping, allowing repeat analyses on
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   The present invention relates to a composition comprising two nucleic acids each containing an electron-transfer group (ETM) having different redox potentials. The invention is used for electronic detection of nucleic acids, especially of substitutions (mismatches) and single-nucleotide polymorphisms, e.g. for genotyping, monitoring gene expression.
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Electron-transfer group; ETM; mismatch; genotyping; gene expression; ss.
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.6e-29;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Example 6; Fage 127; 159pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (CLIN-) CLINICAL MICRO SENSORS INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    26-JUL-1999; 99US-0145695.
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This invention describes a novel protein (I) comprising identical or different catalytic domains of glycosyl transferases and which has processive activity (i.e. builds up oliopsaccharide glycolipids by successive addition of glucose units). (I) can be used to produce 3-olioglucosyl-1,2-diacylglycerols useful as food emulsifiers, polymer modifiers or detergents. This sequence encodes a Bacilius subtilis glycosyl transferase catalytic domain which is used in the method of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Catalytic domain; glycosyl transferase; processive activity; detergent; oligosaccharide glycolipid; 3-oligoglucosyl-1,2-diacylglycerol; food emulsifier; polymer modifier; glycosyl transferase; ss.
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Submitted (02-JUN-1999) Genoscope - Centre National de Sequencage BP 191 91006 EVRY cedex - FRANCE (E-mail : segrefégenoscope.cns.fr

JOURNAL

COMMENT

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Print Student Care France (" mmar. " Supersymmetric Carlaboration with the Berkeley Drosophila Genome Project (BDGP). Determination of this BAC-end sequence was carried out as part of collaboration with the Berkeley Drosophila Genome Project (BDGP). The BDGP is constructing a physical map of the Drosophila melanogaster genome using these BACs. For further information please see http://www.fruitfly.org The BDGP Drosophila melanogaster BAC library was prepared by Kazutoyo Osoegawa and Aarop Mammoser in Pieter de Jong's laboratory in the Department of Cancer Genetics at the Roswell Park Cancer Institute in Buffalo, NY. The library is named RPCI-98 and was constructed by partial ECORI digestion of Drosophila DNA provided by the BDGP from the isogenic strain y2; cn bw sp, the same strain used for the BDGP's pand how to order individual BAC clones, the entire library and how to order individual BAC clones, the entire library and how to order individual BAC clones, the entire library. In coation/Qualifiers

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Submitted (12-APR-2000) to the EWBL/GenBank/DDBJ databases
This sequence is a single read and was generated as part of a large
scale clone-end sequencing project of the Tetraodon nigroviridis
genome. For more information, please take a look at
http://www.genoscope.cns.fr/Tetraodon.
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                                                                                                                                                                                               Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei; Acanthonorpha; Acanthopterygii; Percomorpha; Tetraodontiformes; Tetraodontidae; Tetraodon.

1 (bases 1 to 976)

1 (bases 1 to 976)

2 (bases 1 to 976)

Bouncau,L., Billault,A., Quetier,F., Saurin,W., Bernot,A. and Weissenbach,J.
                                                                                                                                                                                                                                                                                                                                                                                          2 (bases 1 to 976)
Roest-Crollius, ". Jaillon, O., Dasilva, C., Bouneau, L., Fisher, C.,
Bernot, A., Fizames, C., Wincker, P., Brottier, P., Quetier, F.,
Saurin, W. and Welssenbach, J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                           Human gene number estimate provided by genome wide analysis using Tetraodon nigroviridis DNA sequence
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                                                CNSO4E5M 976 bp DNA GSS 21-MAY-2000
Tetraodon nigroviridis genome survey sequence T7 end of clone
103P02 of library G from Tetraodon nigroviridis, genomic survey
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/db_xref="taxon:99883"
/clone=1103P02"
/clone_lib="G"
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AL286627 GI:8025084
GSS; genome survey sequence.
Tetraodon nigroviridis
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Determination of this BAC-end sequence was carried out as part of collaboration with the Berkeley Drosophila Genome Project (BDGP). The BDGP is constructing a physical map of the Drosophila melanogaster genome using these BACs. For further information please see http://www.fruitfly.org The BDGP Drosophila melanogaster BAC library was prepared by Kazutoyo Osoegawa and Aaron Mammoser in Pieter de Jong's laboratory in the Department of Cancer Genetics at the Roswell Park Cancer Institute in Buffalo, NY. The library is named RECI-98 and was constructed by partial EcoRI digestion of prosophila DNA provided by the BDGP from the isogenic strain y2; cn bw sp, the same strain used for the BDGP's pl and EST libraries. A more detailed description of the library, and how to order individual BAC clones, the entire library, or filters for hybridization from the BACPAC Resource Center can be location/Qualifiers
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Submitted (02-JUN-1999) Genoscope - Centre National de Sequencage
BP 191 91006 EVRY cedex - FRANCE (E-mail : segref@genoscope.cns.fr
                                Drosophila melanogaster genome survey sequence TET3 end of BAC \sharp BACR08K10 of RPCI-98 library from Drosophila melanogaster (fruit
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Eukaryota: Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
Pterygota: Neoptera; Endopterygota; Diptera; Brachycera;
Muscomorpha; Ephydroidea; Drosophilldae; Drosophila.
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/db_xref="taxon:7227"
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Submitted (02-JWN-1999) Genoscope - Centre National de Sequencage :
BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr
- Web : www.genoscope.cns.fr)

Public september of this BAC-end sequence was carried out as part of a collaboration of this BAC-end sequence was carried out as part of a collaboration with the Berkeley Drosophila Genome Project (BDGP).
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Drosophila melanogaster genome survey sequence T7 end of BAC:
BACR39P05 of RPCI-98 library from Drosophila melanogaster (fruit Ily), genomic survey sequence.
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Pterzygota; Neoptera; Endopterygota; Diptera; Brachycera;
Muscomorpha; Ephydroidea; Drosophilldae; Drosophila.
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/db.xref="Laxon:7227"
/clone_lib="RPCI-98"
/clone="BACR39PO5"
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Drosophila melanogaster genome survey sequence T7 end of BAC:
BACR?9B23 of RPCI-98 library from Drosophila melanogaster (fruit
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Muscomorpha; Ephydroidea; Drosophilldae; Drosophila.
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Submitted (02-JUN-1999) Genoscope - Centre National de Sequencage
BP 191 91006 EVRX cedex - FRANCE (E-mail: seqref@genoscope.cns.fr
- Web : www.genoscope.cns.fr)
Determination of this BAC-end sequence was carried out as part of
collaboration with the Berkeley Drosophila Genome Project (BDGP).
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/db_xref="traxon:727"
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The BDGP is constructing a physical map of the Drosophila melanogaster genome using these BACs. For further information please see http://www.fruitfly.org The BDGP brosophila melanogaster BAC library was prepared by Kazutoyo Osoegawa and Aaron Mammoser in Pieter de Jong's laboratory in the Department of Cancer Genetics at the Roswell Park Cancer Institute in Buffalo, NY. The library is named RPCI-98 and was constructed by partial EcoRI digestion of Drosophila DNA provided by the BDGP from the isogenic strain v2: or bw sp, the same strain used for the BDGP's pl and EST libraries. A more detailed description of the library and how to order individual BAC clones, the entire library or fillers for hybridization from the BACPAC Resource Center can be found at http://bacpac.med.buffalo.edu/drosophila_bac.htm.
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/db_xref="taxon:7227"
/clone_lib="RPCI-98"
/clone="BACR29B33"
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31.5%; Pred. No. 0.0065;
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Petron of this BAC-end sequence was carried out as part of a collaboration of this BAC-end sequence was carried out as part of a collaboration of this BAC-end sequence was carried out as part of a collaboration with the Berkeley Drosophila Genome Project (BDGP). The BDGP is constructing a physical map of the Drosophila melanogaster genome using these BACs. For further information please see http://www.fruitfly.org The BDGP Drosophila melanogaster BAC library was prepared by Kazutcyo Osoegawa and Aaron Mammoser in Pieter de Jong's laboratory in the Department of Cancer Genetics at the Roswell Park Cancer Institute in Buffalo, NY. The library is named RPCI-98 and was constructed by partial ECORI digestion of Drosophila DNA provided by the BDGP from the isogenic strain y2; on bw sp, the same strain used for the BDGP's pl and EST libraries. A more detailed description of the library and how to order individual BAC clones, the entire library, or filters for hybridization from the BACPAC Resource Center can be location/Qualifiers
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                                                                                                                                                                                                                                                                                                                     Submitted (02-JUN-1999) Genoscope - Centre National de Sequencage
BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr
  RPCI-98 library from Drosophila melanogaster (fruit
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       165 tatttgtaaaaaatggtatatcaatagctttaaatattttagaaatatgtacaaagggtt 224
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                                                                                                                                           Drosophila melanogaster
Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Inse
Pterygota; Neoptera; Endopterygota; Diptera; Brachycera;
Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.
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/db_xref="taxon:7227"
/clone_lib="RPCI-98"
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Local Similarity 38.1%; Pred. No. 0.011;
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                       fly), genomic survey sequence.
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Determination of this BAC-end sequence was carried out as part of a collaboration with the European Drosophila Genome Project (EDGP) - http://www.edgp.ebi.ac.uk -. This Drosophila melanogaster BAC library (Dros BAC) was made by Alain Billaud at CEPH (Centre d'Etude du Polymorphisme Humain) with funding provided by a MRC project grant. The DNA was prepared from embryos by Alain Bucheton and Genevieve Payan. It has been constructed in the vector
                                                                                                                                                                                                                                                                                                                                                                                                                                       Submitted (23-JUL-1999) Genoscope - Centre National de Sequencage BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr
                                                                                      CNS0145P 1043 bp DNA GSS 26-JUL-1999
Drosophila melanogaster genome survey sequence T7 end of BAC
BACN11G11 of DrosBAC library from Drosophila melanogaster (fruit
fly), genomic survey sequence.
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Ptertygota; Neoptera; Endopterygota; Diptera; Brachycera;
Muscòmorpha; Ephydroidea; Drosophilidae; Drosophila.
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1. .1043
/organism="Drosophila melanogaster"
/plasmid="pBeloBAC11"
/db_xref="taxon:7227"
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/clone="BACN11G11"
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Tetracdon nigroviridis.

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

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Acatinopterygii; Teleosteli; Euteleosteli; Neoteleosteli;

Tetracdontidae; Tetracdon.

I (base; Ito 1092)

Roest-Crollius, H., Jaillon, O., Dasilva, C., Fizames, C., Fisher, C.,

Bouncau, L., Billault, A., Quetier, F., Saurin, W., Bernot, A. and

Weissenbach, J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                   2 (bases 1 to 1092)
Roest-Crollius, H., Jaillon, O., Dasilva, C., Bouneau, L., Fisher, C.,
Bernot, A., Fizames, C., Wincker, P., Brottier, P., Quetier, F.,
Saurin, W. and Weissenbach, J.
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t 113 others
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Tetraodon nigroviridis genome survey sequence T7 end of clone
222Lll of library G from Tetraodon nigroviridis, genomic survey
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                 gccgtattcaacaagatattatgtggcaacaaaagaaacgaaacaagacttcatagac
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/db_xref="taxon:99883"
/clone="222111"
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/clone_lib="G"
/note="Genoscope sequence '
165 g 262
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                                                                                                                                                                                                                GSS; genome survey sequence. Tetraodon nigroviridis.
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AL175696.1 GI:7813753
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Submitted (23-JUL-1999) Genoscope - Centre National de Sequencage : BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr )
Determination of this BAC-end sequence was carried out as part of a collaboration with the European Drosophila Genome Project (EDGP) - http://www.edgp.ebi.ac.uk · This Drosophila melanogaster EAC library (Dros BAC) was made by Alain Billaud at CEPH (Centre d'Etded uu Pollymorphisme Humain) with funding provided by a MRC and Genevieve Payan. It has been constructed in the vector
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Drosophila melanogaster genome survey sequence T7 end of BAC and SACNIGD2 of DrossBAC library from Drosophila melanogaster (fruit fly), genomic survey sequence.
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1 (bases 1 to 1101)
Genoscope.
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                                                                                                                                         ctggattacgccgtattcaacaagatattatgtggcaacaaaagaaacgaaacaagactt
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/plasmid="pBeloBAC11"
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31.6%; Pred. No. 0.022;
tive 75; Mismatches 144;
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Plasmid Drosophila melanogaster
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/note="end : T7"
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903 tgcacctggtcaagagettgaaaatgeettttaetttgaagaaaaaggttttggtaa 959

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AW787593 548 bp mRNA EST 16-MAY-2000
945011D04.X2 945 - Mixed adult tissues from Walbot lab, same as 707
AW787593
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Vector: pGAD10; Site_1: EcoRI; cDNA library from fully
differentiated maize tissues from an active Mutator plant.
Tissue ratio is 4:2:1:1:1:1 (tassel, kernel, silk, husk,
root, leaf). Unidirectionally cloned. New library number
given to library 707 for additional sequencing."
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/clone_lib="9457" Mixed adult tissues from Walbot lab, same as 707 (sk).
/tissue_type="tassel, kernal, silk, husk, root, leaf" /dev_stage="fully-grown"
/lab_host="hush-"pilog"
                    263 acaaatactatggacttaataagttaattaatttattgataaaagaaaagccagatttaa 322
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Pred. No. 0.023;
0; Mismatches 76; Indels
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Department of Biological Sciences
Stanford University
855 California Ave, Palo Alto, CA 94304, USA
Tel: 650 723 2227
Fex: 650 725 8221
Email: walbot@stanford.edu
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/organism="Zea mays"
/cultivar="W23" ___
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AW787592 595 bp mRNA EST 16-MAY-2000
945011004.X1 945 - Mixed adult tissues from Walbot lab, same as 707
AW787592
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Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACC
clade; Panicoideae; Andropogoneae; Zea.
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/db.xref="taxon:4577"
/clone_lib="945 - Mixed adult tissues from Walbot lab,
same as 707 (SK)"
/tissue_rype="tassel, kernal, silk, husk, root, leaf"
/lab_host="fully-grown"
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Maige ESTs from various cDNA libraries sequenced at Stanford
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Pred. No. 0.023;
0; Mismatches 76; Indels 0;
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Fax: 650 725 8221
Email: walbot@stanford.edu
Plate: 945011 row: D column: 04.
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Department of Biological Sciences
Stanford University
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Best Local Similarity 57.1;
Matches 101; Conservative
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ORGANISM

KEYWORDS SOURCE

AUTHORS TITLE

JOURNAL

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FEATURES

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Direct Submission

Submitted (02-JUN-1999) Genoscope - Centre National de Sequencage :

BP 191 91006 EVRY cedex - FRANCE (E-mail : seqréfégenoscope.cns.fr - Web : www.genoscope.cns.fr)

Determination of this BAC-end sequence was carried out as part of a collaboration with the Berkeley Drosophila Genome Project (BDGP).

The BDGP is constructing a physical map of the Drosophila melanogaster genome using these BACs. For further information please see http://www.fruitfly.org The BDGP Drosophila melanogaster BAC library was prepared by Kautucoyo Oscogawa and Aaron Mammoser in Pieter de Jong's laboratory in the Department of Cancer Genetics at the Roswell Park Cancer Institute in Buffalo, NY. The library is named RPCI-98 and was constructed by partial EcoRI digestion of Drosophila DNA provided by the BDGP from the isogenic strain y2; cn bw sp, the same strain used for the BDGP's and how to order individual BAC clones, the entire library or filters for hybridization from the BACPAC Resource Center can be found at http://Dacpac.med.buffalo.edu/drosophila_bac.htm.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CNSO20K7 1092 bp DNA GSS 12-MAY-2000
Tetraodon nigroviridis genome survey sequence T7 end of clone
222Lil of library G from Tetraodon nigroviridis, genomic survey
sequence.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /organism="Drosophila melanogaster"
/db_xref="taxon:7227"
/clone_lib="RPCI-98"
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/cultivar="W23"
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/cultivar="W23"
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FECRI; Site_2: XhoI; 3-4 days old root tissue from Walbot
         A1979696 610 bp mRNA EST 30-AUG-1999 614045D09.x4 614 - root cDNA library from Walbot Lab Zea mays cDNA,
                                                                                                                                                                                       Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACC clade; Panicoideae; Andropogoneae; Zea.

1 (bases 1 to 610)
Walbot, V.

Maize ESTs from various cDNA libraries sequenced at Stanford
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Pred. No. 0.023;
0; Mismatches 76; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 others
                                                                                                                                                                                                                                                                                                                                                    Unpublished (1999)
Contact: Walbot V
Contact: Walbot V
Stanford University
855 California Ave, Palo Alto, CA 94304, USA
Fax: 650 723 222
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Plate: 614045 row: D columr
Location/Qualifiers
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364 801

RESULT 14 CNS001FB/C

DEFINITION

LOCUS

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ORGANISM

AUTHORS

REFERENCE

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Submitted (12-APR-2000) to the EMBL/GenBank/DDBJ databases
This sequence is a single read and was generated as part of a large
scale clone-end sequencing project of the Tetraodon nigroviridis
genome. For more information, please take a look at
http://www.genoscope.cns.fr/Tetraodon.
Location/Qualifiers
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                                                                                        Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei; Acanthopterygii; Teleostei; Euteleostei; Neoteleostei; Terandontidae; Tetrandon. Tetrandontidae; Tetrandon. Tetrandon. Tetrandon. Tetrandon. Tetrandon. Tetrandon. Tetrandon. Tetrandon. Hoses 1 to 1092)
Roest-Crollius, H., Jailland, O., Dasilva, C., Fizames, C., Fisher, C., Bouneau, L., Billault, A., Quetler, F., Saurin, W., Bernot, A. and Chardterization and repeat analysis of the compact genome of the freshwater pufferish Tetrandon nigroviridis
                                                                                                                                                                                                                                                                                                                                                                                                  Human gene number estimate provided by genome wide analysis using Tetraodon nigroviridis DNA, sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /organism-Tretracdon nigroviridis"
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/clone=11b="c"
/clone=11b="c"
/note="Genoscope sequence ID : COAG222CF06LP1-end : T7"
a 169 c 165 g 262 t 113 others
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33.7%; Pred. No. 0.033;
Live 64; Mismatches 188; Indels
                                   GSS; genome survey sequence.
Tetraodon nigroviridis.
Tetraodon nigroviridis
                    AL175696.1 GI:7813753
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Search completed: June 29, 2001, 10:55:58 Job time: 5021 sec

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Sequence Sequence Sequence S

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APPLICANT: Wallis, Nicola G.
TITLE OF INVENTION: MATE
TITLE OF SEQUENCES: 6
CORRESPONDENCE ADDRESS:
ADDRESSEE: Dechert Price & Rhoads
STREET: 4000 Bell Atlantic Tower, 1717 Arch Stre
CITY: Philadelphia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          44.8%; Score 437; DB 3; I
100.0%; Pred. No. 5.5e-97;
ive 0; Mismatches 0;
US-08-645-1938-18
US-08-998-416-595
US-08-998-416-595
US-08-724-394A-21
US-08-724-394A-22
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US-08-724-394A-22
US-08-724-394A-22
US-08-933-08386-7
PCT-US93-08386-1
US-08-998-416-1934
US-08-998-416-1934
US-08-998-416-1934
US-08-998-416-920
US-07-991-8678-8
US-07-991-8678-8
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US-08-998-416-1137
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SOFTWARE: FastSEO for Windows Version 2.0 CURRENT APPLICATION DATA: APPLICATION NUMBER: US/08/988,251
                                                                                                                                                                                                                                                                                                                                                                                                                                                          ALIGNMENTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            REFERENCE/DOCKET NUMBER: GM10094
TELECOMUNICATION INFORMATION:
TELEPHONE: 215-994-2252
TELEFAX: 215-994-222
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           US-08-988-251-1/c
; Sequence 1, Application US/08988251
; Patent No. 6013497
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PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
-ATTORNEY/AGENT INFORMATION:
NAME: DICKINSON, TOOM OREGISTRATION NUMBER: 28,35
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDIUM TYPE: Diskette
COMPUTER: IBM COMPATIBLE
OPERATING SYSTEM: DOS
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LENGTH: 2600 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
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Matches 437; Conservative
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COMPUTER READABLE FORM:
MEDIUM TYPE: Diskett
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  US-08-988-251-1
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                                                                                                                                             June 29, 2001, 11:46:43; Search time 119.12 Seconds (without alignments) 1516.360 Million cell updates/sec
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/cgn2_6/ptodata/1/ina/5B_COMB.seq:*
/cgn2_6/ptodata/1/ina/6A_COMB.seq:*
/cgn2_6/ptodata/1/ina/6B_COMB.seq:*
/cgn2_6/ptodata/1/ina/PCTUS.COMB.seq:*
/cgn2_6/ptodata/1/ina/PCTUS.COMB.seq:*
                GenCore version 4.5 . Copyright (c) 1993 - 2000 Compugen Ltd.
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US-08-487-8268-13

US-08-487-8268-13

US-08-49-391-11

US-09-390-200-11

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US-08-91-17-9

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US-08-801-028-95
US-09-340-154-95
PCT-US95-09338-95
PCT-US95-09339-95
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US-08-392-625-16
US-08-466-961A-16
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Maximum Match 100%
Listing first 45 summaries
                                                                                                         - nucleic search, using sw model
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Gapop 10.0 , Gapext 1.0
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length: 200000000
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Gaps 9

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Length 2600; Indels 360 198

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APPLICANT: O'Sullivan, William J
TITLE OF INVENTION: Nucleotide sequence encoding carbamoyl
TITLE OF INVENTION: phosphate synthetase II
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 46.4; DB 2; Length 8
Pred. No. 0.015;
0; Mismatches 161; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ADDRESSEE: Nixon & Vanderhye PC
STREET: 1100 No. 5849573th Glebe Road, 8th Floor
CITY: Arlington
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.24
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/446,855A
FILING DATE: 06-Jul-1995
                                                                                                                                                                                                                                                                                                                           ; Sequence 1, Application US/08446855A; Patent No. 5849573
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Mitchard, Leonard C
REGISTRATION NUMBER: 29.009
REFRENCE/DOCKET NUMBER: 47-8
TELECOMMUNICATION INFORMATION:
TELEPHONE: 703-816-4000
TELEPAX: 703-816-4100
                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: Stewart, Thomas S
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  4.88;
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Matches 155; Conservative
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
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557 ATGGTTACTCAAAATAAAAAGATATTGATTATTACTGGCTCATTCGGTAACGGTCATATG 498
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: Walling, Lisa
APPLICANT: Shilling, Lisa
APPLICANT: Sabelerowski, Susan
TITLE OF INVENTION: MurE
FILE REFERENCE: GMI0094-D1
CURRENT FILING DATE: 1999-08-30
EARLIER APPLICATION NUMBER: US 08/988,251
EARLIER APPLICATION NUMBER: US 60/059,956
EARLIER FILING DATE: 1997-12-10
EARLIER APPLICATION NUMBER: US 60/059,956
EARLIER FILING DATE: 1997-09-25
NUMBER OF SEQ ID NOS: 6
SOFTWARE: FastSEQ for Windows Version 4.0
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100.0%; Pre/
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Patent No. 6103507
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                                                                                                                                                                                                                                                                                                                                                                                 Conservative
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Best Local Simi
Matches 437;
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4.6%; Score 44.8; DB 1; Length 7
Best Local Similarity 6.3%; Pred. No. 0.034;
Matches 25; Conservative 203; Mismatches 170; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER: LLD. COMPUTER: PC-DOS/MS-DOS SOFTWARE: Patentin Release #1.0, Version #1.25 CURRENT.APPLICATION DATA:

APPLICATION NUMBER: US/08/232,463
FILING DATE: CASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION DATA:
APPLICATION DATA:
APPLICATION NUMBER: US/07/935,313
                                                                                                                                                                              FOWLPOX VIRUS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FILING DATE:
APPLICATION NUMBER: EP 91 114 300.6
FILING DATE: 126-A0C1991
ATTORNEY AGENT INFORMATION:
NAME: BENT, Stephen A.
REGISTRATION NUMBER: 29,768
REFERENCE/DOCKET NUMBER: 30472/114 IMMU
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703)836-9300
TELEFAX: (703)683-4109
                                                                                                                                                                                                                                                               Suite 500
                                                                                                         APPLICANT: DORNER, F.
APPLICANT: SCHETELINGER, F.
APPLICANT: FALKNER, F. G.
TITLE OF INVENTION: RECOMBINANT FO
NUMBER OF SEQUENCES: 52
CORRESPONDENCE ADDRESS:
ADDRESSEE: FOLEY & LARGHER
                                           Sequence 14, Application US/08232463
Patent No. 5670367
                                                                                                                                                                                                                                          ADDRESSEE: Foley & Lardner
STREET: 1800 Diagonal Road,
CITY: Alexandria
                                                                                                                                                                                                                                                                                                                                                                        COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                7218 base pairs
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
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STRANDEDNESS: | single
                                                                                                                                                                                                                                                                                      CIII.
STÂTE: Va
STÂTE: Va
COUNTRY: USA
COUNTRY: USA
Z2313-0299
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US-08-232-463-14
                                                                                       GENERAL INFORMATION:
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IMMEDIATE SOURCE:
  RESULT 5
US-08-232-463-14/C
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                      8562 ttacgitiaaatattaataaaigittitaitaaaatagaicaitaatttatatigaitta 8621
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                                                                                                                                                                          307 gaaaagccagatttaattattattaacgtttcctacaccagttatgtcggtactaactgag 366
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        tagottttaaatattttagaaatatgtacaaagggttttattacagocogoccagataaact 248
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                                                                                                                                                                                                                                                                                                                                                                                                                                                    GENERAL INFORMATION:
APPLICANT: Stewart et al.
TITLE OF INVENTION: Nucleotide Sequence Encoding Carbamoyl Phosphate
Patent No. 6183996
TITLE OF INVENTION: Synthetase II
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     5;
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4.8%; Score 46.4; DB 4; Length 8920;
Best Local Similarity 48.7%; Pred. No. 0.015;
Matches 155; Conservative 0; Mismatches 161; Indels 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FILE REFERENCE:
CURRENT APPLICATION NUMBER: US/09-430, 741
CURRENT FILING DATE: 1998-09-10
EARLIER APPLICATION NUMBER: PL6380
EARLIER PILING DATE: 1992-12-16
EARLIER FILING DATE: 1993-12-02
EARLIER FILING DATE: 1993-12-02
EARLIER FILING DATE: 1993-10-02
EARLIER FILING DATE: 1995-07-06
NUMBER OF SEQ ID NOS: 15
SOFTWARE: PatentIn Ver. 2.0
                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 1, Application US/09150741
Patent No. 6183996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ; TYPE: DNA
; ORGANISM: Plasmodium falciparum
US-09-150-741-1
                                                                                                                                                                                                                                                                                                      8802 AAATGTTATGATTTTTT 8819
                                                                                                                                                                                                                                                            367 caatttaacattaatt 384
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LENGTH: 8920
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Length 7218;

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GENERAL INFORMATI
                                                                                                                                                                                                                                                      US-08-487-826B-13/C
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US-08-487-826B-13
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SOFTWARE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
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AND PLASMODIUM FALCIPARUM ERYTHROCYTE BINDING PROTEINS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ij
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              66 tacacagagtatcgttaatcaacttaatgatatgaatctagaccatttaagcgtcattga 125
                                                                                          612 tattttaatgtcagctggtgcatttggtgtatctaaaggttttgacacgatgattactga 671
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           6 tactcaaaataaaaagatattgattattactggctcattcggtaacggtcatatgcaagt
                                                                      672 tatattagcgaaaagtgcaaatgcacaagtagttatgatttgtggtaagagcaaagagct
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SOFTWARE: Patentin Release #1.0, Version #1.25 CURRENT APPLICATION DATA: APPLICATION NUMBER: US/08/487,826B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         0; Mismatches 147;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      8; DB 2;
0.075;
                                                                                                                                                               ADDRESSEE: Knobbe Martens Olson & Bear
STREET: 620 Newport Center Drive 16th Floor
CITY: Newport Beach
STATE: California
                                                                                                                                      732 aaagcgttctttaacagctaagtttaaattaacgagaa 769
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Pred. No. 0.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    имьек: US/08/487,826в
10-sep-1993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ZIP: 92660
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
CMMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                       Sequence 13, Application US/08487826B Patent No. 5993827
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ATTORNEY AGENT INFORMATION:
NAME: Israelsen, Ned
REGISTATION UNDBER: 29,655
REFERENCE/DOCKET NUMBER: NIH12
TELECOMMUNICATION INFORMATION:
TELEPHONE: (619) 235-8550
TELEFAX: (619) 235-0176
INFORMATION FOR SEQ ID NO: 13:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                         APPLICANT: Miller, Louis H. APPLICANT: Peterson, David S. APPLICANT: Su, Xin-zhaun APPLICANT: Wellems, Thomas E. TITLE OF INVENTION: BINDING DOM NUMBER OF SEQUENCES: 45 CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LENGTH: 19124 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                            Sim, Kim L.
Chitnis, Chetan
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity
Matches 143; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TOPOLOGY: Linear MOLECULE TYPE: CD
                                                                                                                                                                                                                                                                                                GENERAL INFORMATION:
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US-08-487-826B-13
                                                                                                                                                                                                                                           US-08-487-826B-13
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APPLICANT: Sim, Kim L.
APPLICANT: Chitnis, Chetan
APPLICANT: Miler, Louis H.
APPLICANT: Miler, Louis H.
APPLICANT: Willer, Louis H.
APPLICANT: Wellems, Thouns E.
TITLE OF INVENTION: BINDING DOMAINS FROM PLASMODIUM VIVAX
TITLE OF INVENTION: AND PLASMODIUM FALCIPARUM ERYTHROCYTE BINDING PROTEINS
NUMBER OF SEQUENCES: 45
ANDRESPONDENCE ADDRESS:
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                                      132 tttatttatggaageteatecaattttgaettetatttgtaaaaaatggtatateatag 191
                                                                              186 caatagotttaaatattttagaaatatgtacaaagggttttattacagccgcccagataa 245
126 gcacgatttatttatggaagctcatccaattttgacttctatttgtaaaaaatggtatat 185
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                                                                                                                                                                                        Score 42; DB 2; Length 19124; Pred. No. 0.2; 0; Mismatches 145; Indels
                                                                                                                                                            PatentIn Release #1.0, Version #1.25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ADDRESSEE: Knobbe Martens Olson & Bear STREEF: 620 Newport Center Drive 16th Floor STRIEF: Newport Beach STRATE: California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               JO-SEP-1993
                                                                                                                                                                                                                                                                                                          Application US/08487826B
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TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TELEFAX: (619) 235-0176
INFORMATION FOR SEQ ID NO: 13:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (619) 235-8550
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Best Local Similarity 47.1%;
Matches 129; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Israelsen, Ned
REGISTRATION NUMBER: 29,6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LENGTH: 19124 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CURRENT APPLICATION DATA:
APPLICATION NUMBER: US
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   nucleic acid
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STRANDEDNESS:
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61 caagttacacagagtatcgttaatcaacttaatgatatgaatctagaccatttaagcgtc 120
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                                                                                                                                                                                                                                                            121 attgagbacgatttatttattggaageteatecaattttgaettetatttgtaaaaaatgg 180
                                                                                                                                                                                                                                                                                                                                               181 tatatcaatagetttaaatattttagaaatatgtacaaagggttttat-tacageegeee 239
                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 atggttactcaaaataaaaagatattgattattactggctcattcggtaacggtcatatg 60
                                                                                                                               240 agataaactagacaaatgtttttacaaatactatggacttaataagttaatttatt
    Score 41; DB 2; Length 2058;
Pred. No. 0.21;
0; Mismatches 185; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: Cheng, Kuo-Joan
APPLICANT: Cheng, Kuo-Joan
APPLICANT: Selinger, Leonard B.
APPLICANT: Hu, Vouji
APPLICANT: Hu, Youji
APPLICANT: Holoney, Maurice M.
TITLE OF INVENTION: A Xylanase Obtained From an
TITLE OF INVENTION: Anaerobic Fungus
NUMBER OF SEQUENCES: 6
CORRESPONDE, CARESEE Greenlee, Winner and Sullivan, P.C.
STREET: 5370 Manhattan Circle, Suite 201
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           OPERATING SYSTEM: PC DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
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APPLICATION NUMBER: US/08/749,391
FILING DATE: 13-NOY-1996
ATTORINEY/AGENT INFORMATION:
NAME: Doing M. Ferber
REGISTRATION NUMBER: 33,878
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICATION NUMBER: US/09/390,200
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ZIP: 80803 |
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 1, Application US/09390200 Patent No. 6137032
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TELECOMMUNICATION INFORMATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TELEFAX: (303) 499-8080
TELEFAX: (303) 499-8089
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 2058 base pairs
TYPE: nucleic acid
  Query Match
Best Local Similarity 46.73
Matches 163; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CITY: Boulder
STATE: Colorado
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 US-09-390-200-1
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252 caaatgittitacaaatactatggacttaataagttaattaatttattgataaaagaaaa 311
                                                                312 gccagatttaatattattaacgtttcctacaccagttatgtcggtactaactgagcaatt
                                                                                                                                                                                                                                                                                                                                                                                              GENERAL INCORMATION:
APPLICANT: Cheng, Kuo-Joan
APPLICANT: Cheng, Kuo-Joan
APPLICANT: Selinger, Leonard B.
APPLICANT: Liu, Jin-Hao
APPLICANT: Hu, Youlj
APPLICANT: Ho, Youlj
APPLICANT: Moloney, Maurice M.
TITLE OF INVENTION: A Xylanase Obtained From an
TITLE OF INVENTION: Anaerobic Fungus
NUMBER OF SEQUENCES: 6
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/749,391
FILING DATE: 13.NOV-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             E: Greenlee, Winner and Sullivan, P.C. 5370 Manhattan Circle, Suite 201
                                                                                                                                                                                                                                                   6855 TATTATTTTTTATGTTTTATTTAAGTAAA 6822
                                                                                                                                                                                                               372 taacattaatattccagttgctacagtgatgaca 405
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ORGANISM: Neocallimastix patriciarum STRAIN: 27
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ZIP: 80803
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
MEDIUM TYPE: Floppy disk
MEDIUM TYPE: Ploppy disk
MEDIUM TYPE: Ploppy disk
                                                                                                                                                                                                                                                                                                                                                                 Sequence 1, Application US/08749391
Patent No. 5948667
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LIBRARY: genomic DNA library CLONE: pNspx-06
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ATTORNEY/AGENT INFORMATION:
NAME: Donna M. Ferber
REGISTRATION NUMBER: 33,878
REFERENCE/DOCKET NUMBER: 93.
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TELEPHONE: (303) 499-8080
TELEFAX: (303) 499-8089
INPORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MOLECULE TYPE: DNA (genomic)
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TYPE: nucleic acid
STRANDEDNESS: double
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CLASSIFICATION:
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; LOCATION: 301.
US-08-749-391-1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ANTI-SENSE: NO
ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      HYPOTHETICAL:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ADDRESSEE:
                                                                                                                                                                                                                                                                                                                      RESULT 8
US-08-749-391-1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          121 attgagcacgatttatttatggaagctcatccaattttgacttctatttgtaaaaaatgg 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 181 tatatcaatagctttaaatattttagaaatatgtacaaagggttttat-tacagccgccc 239
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            189 GGAATTATTTACTTTCACTGGTGGAAACAAAATATTAATAGTGTATAATATTATTAGAA 248
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 atggttactcaaaataaaaagatattgattattactggctcattcggtaacggtcatatg 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: Ohno, Tsuneya
APPLICANT: Ohno, Tsuneya
APPLICANT: Matsuhisa, Akio
APPLICANT: Beda, Soji
TITLE OF INVENTION: Probe for Diagnosing Infectious Disease
NUMBER OF SEQUENCES: 25
CORRESPONDENCE ADDRESS:
ADDRESSE: Marshall, O'Toole, Gerstein, Murray & Borun
STREET: 6300 Sears Tower, 233 South Wacker Drive
                                                                                                                                                                                                                                                                                                                                  Score 41; DB 4; Length 2058;
Pred. No. 0.21;
0; Mismatches 185; Indels
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                                                                                                                  Neocallimastix patriciarum
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CITY: Chicago
STATE: 1111nois
COUNTRY: United States of America
ZIP: 60606-6402
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICATION NUMBER: US/08/920,812
FILING DATE: 29-AUG-1997
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 US-08-920-812-6/c

; Sequence 6, Application US/08920812

; Patent No. 5763188

; GENERAL INFORMATION:
                                                                                                                                                                          LIBRARY: genomic DNA library CLONE: pNspX-06
                                   MOLECULE TYPE: DNA (genomic) HYPOTHETICAL: NO
                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity 46.7%;
Matches 163; Conservative
double
                                                                                                                                                                                                                                    CDS
301..1755
                  linear
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                                                   HYPOTHETICAL: NO
ANTI-SENSE: NO
ORIGINAL SOURCE:
ORGANISM: NEOC
                                                                                                                                                       IMMEDIATE SOURCE:
                                                                                                                                                                                                                                                       ;
US-09-390-200-1
                                                                                                                                                                                                                                    NAME/KEY:
                                                                                                                                    STRAIN:
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1648 TAAAAAAATCGATGATTTACTTAAACGAGTAAACAACCGTATCACAGAAGCAAATAATGA 1589
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APPLICANT: Matsuhisa, Akio
APPLICANT: Uehara, Hirotsugu
APPLICANT: Eda, Soji
TITLE OF INVENTION: Probe for Diagnosing Infectious Disease
NUMBER OF SEQUENCES: 25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 4.1%; Score 40; DB 1; Length 8654; 52.1%; Pred. No. 0.51; tive 0; Mismatches 81; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             315 agatttaatattattaacgtttcctacaccagttatgtcggtactaact
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              5: Marshall, O'Toole, Gerstein, Murray & 6300 Sears Tower, 233 South Wacker Drive
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Version #1.25
                                                                                                                                                                                                                                                                                                                                                                          ); ORGANISM: Staphylococcus epidermidis
; STRAIN: Clinical Isolate SE-22
US-08-920-812-6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/362,577
FILING DATE: 27-WAR-1995
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CITY: Chicago
STATE: Illinois
COUNTRY: United States of America
ZIP: 60606-6402
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SOFTWARE: Patentin Release #1.0,
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/920,827
FILING DATE: 29-AUG-1997
    US 08/362,577
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 6, Application US/08920827
Patent No. 5770375
                                                              NAME: Rin-Laures, Li-Hsien
REGISTRATION NUMBER: 33.547
REFERENCE/DOCKET NUMBER: 19
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Rin-Laures, Li-Hsien
                                                                                                                                                  TELEPHONE: 312/474-6300
TELEFAX: 312/474-0448
TELEX: 25-3856
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 8654 base pairs
APPLICATION NUMBER: US 08 FILING DATE: 27-MAR-1995 ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                               Genomic DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity 52.18
Matches 88; Conservative
                                                                                                                                                                                                                                                                                                           double
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                                                                                                                                                                                                                                                                                  TYPE: nucleic acid STRANDEDNESS: doub
                                                                                                                                                                                                                                                                                                                             linear
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                                                                                                                                                                                                                                                                                                                          TOPOLOGY: line MOLECULE TYPE: GORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ADDRESSEE:
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US-08-920-827-6/c
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1648 TAAAAAATCGATGATTTACTTAAACGAGTAAACAACCGTATCACAGAAGCAAATAATGA 1589
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 40; DB 1; Length 8654;
Pred. No. 0.51;
0; Mismatches 81; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            315 agatttaatattaacgtttcctacaccagttatgtcggtactaact 363
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MEDIUM TYEE: Floppy disk
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CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/362,577C
FILING DATE: 27-MAR-1995
CLASSIFICATION: 536
                                                                                                                                                                                                                                                                                                       ORGANISM: Staphylococcus epidermidis
STRAIN: Clinical Isolate SE-22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PC-DOS/MS-DOS
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Patent No. 5807673
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GENERAL INFORMATION:
APPLICANT: Ohno, Tsuneya
APPLICANT: Matsuhisa, Akio
APPLICANT: Welara, Hirotsugu
APPLICANT: Eda, Soll
TITLE OF INVENTION: Probe for INVENTION:
NUMBER OF SEQUENCES: 25
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      REFERENCE/DOCKET NUMBER: 19
TELECOMMUNICATION INFORMATION
TELEPHONE: 312/474-6300
TELEFAX: 312/474-0448
                                     INFORMATION FOR SEQ ID NO: 6: SEQUENCE CHRACTERISTICS: LENGTH: 8654 base pairs TYPE: nucleic acid STRANDEDNESS: double TOPOLOGY: linear MOLECULE TYPE: Genomic DNA ORIGINAL SOURCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NAME: Rin-Laures, Li-Hsien
REGISTRATION NUMBER: 33,54
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity 52.1%;
Matches 88; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Genomic DNA
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TELEX: 25-3856
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
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STRANDEDNESS: | double
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        OPERATING SYSTEM:
SOFTWARE: PatentI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MOLECULE TYPE:
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                                                                                                                                                                                                                                                                                                                                             ; STRAIN:
US-08-921-177-6
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                    TELEX:
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Patent No. 579821
GENERAL INFORMATION:
APPLICANT: Onno, Tsuneya
APPLICANT: Onno, Tsuneya
APPLICANT: Uchara, Hirotsugu
APPLICANT: Bda, Soji
TITLE OF INVENTION: Probe for Diagnosing Infectious Disease
NUMBER OF SEQUENCES: 25
CORRESPONDENCE ADDRESS:
ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
STREFT: 6500 Sears Tower, 233 South Wacker Drive
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 40; DB 1; Length 8654;
Pred. No. 0.51;
0; Mismatches 81; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              315 agatttaatattattaacgtttcctacaccagttatgtcggtactaact 363
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REGISTRATION NUMBER: 33,547
REFERENCE/DOCKET NUMBER: 19036/32420
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312/474-6300
TELERAX: 312/474-0448
TELEX: 25-3856
INFORMATION FOR SEQ ID NO: 6: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                          ; ORGANISM: Staphylococcus epidermidis
; STRAIN: Clinical Isolate SE-22
US-08-920-827-6
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STATE: 1111nois
COMPUTEY: United States of America
ZIP: 60606-6402
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
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APPLICATION NUMBER: US 08/362,577
ELLING DATE: 27-MAR-1995
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NAME: Rin-Laures, Li-Hsien
REGISTRATION NUMBER: 33,547
REFERENCE/DOCKET NUMBER: 19
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312/474-6300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Ouery Match 4.1%;
Best Local Similarity 52.1%;
Matches 88; Conservative
                                                                                                                                                                                                                                                                                                                                                                  TOPOLOGY: linear
MOLECULE TYPE: Genomic DNA
ORIGINAL SOURCE:
                                                                                                                                                                                                                                             QUENCE CHANNEL BASE pairs
LENGTH: 8654 base pairs
TYPE: nucleic acid
CTANNENNESS: double
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                                                                                                                                                                                                                                           1648 TAAAAAAATCGATGATTTACTTAAACGAGTAAACAACCGTATCACAGAAGCAAATAATGA 1589
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                                                                                                                                                                                                                                                                                   195 taaatattttagaaatatgtacaaagggttttattacagccgcccagataaactagacaa 254
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                                                                                                                                                                                                                                                                                                                                                                                                    1528 TGTTTTACTCTTTTATTAAGTTAATACGATAGTGATCTGAGTCCAAACT 1480
                                                                                                                     DB 1; Length 8654;
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                                                                                                                                                             81; Indels
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION UNMBER: US/08/920,828
FILING DATE: 29-AUG-1997
                                                                                                                                                               Mismatches
                                                                                                                     Score 40;
Pred. No. (
                    : Staphylococcus epidermidis
Clinical Isolate SE-22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    : Staphylococcus epidermidis
Clinical Isolate SE-22
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COUNTRY: United States of America
ZIP: 60606-6402
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        US 08/362,577
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 6, Application US/08920828
Patent No. 5853998
GENERAL INFORMATION:
APPLICANT: Ohno, Tsuneya
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/362
FILING DATE: 27-MAR-1995
ATTORNEY/AGENT INFORMATION:
NAME: Rin-Laures, Li-Hsien
REGISTRATION NUMBER: 33,547
                                                                                                                                                             ;
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APPLICANT: Mtsuhisa, Akio
APPLICANT: Uchara, Hirotsugu
APPLICANT: Eda, Soji
TITLE OF INVENTION: Probe for
NUMBER OF SEQUENCES: 25
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   REFERENCE/DOCKET NUMBER: 19
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312/474-6300
TELEFAX: 312/474-0448
                                                                                                                     4.1%;
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: Genomic DNA
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                                                                                                                                                               Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TELEX: 25-3856
INFORMATION FOR SEQ ID NO:
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EDNESS: double
                                                                                                                     Query Match
Best Local Similarity
Matches 88; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STREET: 6300 Se
CITY: Chicago
STATE: Illinois
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ORIGINAL SOURCE:
ORIGINAL SOURCE:
ORGANISM: Sta
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STRANDEDNESS:
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                                     ; STRAIN: CUS-08-362-577C-6
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CONSTRUCTS, PROTEIN PRODUCTS DERIVING THEREFROM, AND
METHODS OF MAKING AND USING SAME
                                                                                                                                                                                  1648 TAAAAAAATCGATGATTTACTTAAACGAGTAAACAACCGTATCACAGAAGCAAATAATGA 1589
                                                                                  195 taaatattttagaaatatgtacaaagggttttattacagccgcccagataaactagacaa 254
                                                                                                                                                                255 atgittittacaaatactatggacttaataagttaattaatttattgataaaagaaaagcc 314
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Pred. No. 0.45;
0; Mismatches 201; Indels
                                           81; Indels
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    DB 2;
                                         0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CLASSIFICATION: 536
ATTORNEY/AGENT INFORMATION:
NAME: WALKER, BARBARA W.
REGISTRATION NUMBER: 35,400
REFERENCE/DOCKET NUMBER: 2093-117A
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202)783-6040
  Score 40;
Pred. No. (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               OPERATING SYSTEM: DOS
SOFTWARE: WordPerfect 5.1+
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/505,486
FILING DATE: 21-UUL-1995
CLASSIFFCATION: 536
PRIOR APPLICATION DATA:
APPLICATION NUMBER: U.S. 08/279,472
FILING DATE: 22-UUL-1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               08/279,472
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ... KUTHWELL, FIGG, ERNST & STREET: 555 Thirteenth Street N.W. CITY: Washington
                                                                                                                                                                                                                                                                                                                                                                             Sequence 96, Application US/08505486
Patent No. 5955573
GENERAL INFORMATION:
TITLE OF INVENTION: UBIQUIN-LYTIC
TITLE OF INVENTION: METHODS OF MAKI
TITLE OF INVENTION: METHODS OF MAKI
NUMBER OF SEQUENCES: 98
CORRESPONDENCE ADDRESS:
ADDRESSEE: ROTHWELL, FIGG, ERNST
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TYPE: NUCLEIC ACID
STRANDEDNESS: DOUBLE STRANDED
4.1%;
milarity 52.1%;
Conservative 0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity 45.3
Matches 167; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER READABLE FORM: MEDIUM TYPE: DISKETT
  Ouery Match
Best Local Similarity
Matches 88; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LINEAR
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US-08-505-486-96
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MOLECULE TYPE:
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326 GAANTATTATTATTACTATATTGCATATAAAACTCAATCAATGGAATAATAATAATGG 267
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                                     266 GTTINNNTIGIGICICICALTATATGAAAAACATIGAAGTIGCTIACIATICAATT 207
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Search completed: June 29, 2001, 11:47:46 Job time: 6678 sec

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June 29, 2001, 08:59:02; Search time 35.83 Seconds (without alignments) 661.568 Million cell updates/sec
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1 WYTQNKKILIITGSFGNGHM.....SSQPQEIYGKVPLYARFFVK 391
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| SIDS8/gcgdata/geneseq/geneseqp/AA1991.DAT:#
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GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
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                                                                                                                                                                                                                                                                                                                                                                                                                             412676 seqs, 60623988 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
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Gapop 10.0 , Gapext 0.5
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Maximum DB seq length: 2000000000
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Perfect score:
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

Description	B. subtilis alvos	Amino acid sequenc	Amino acid sequenc	Monogalactosyldiac	Amino acid sequenc	Amino acid sequenc	Arabidopsis thalia	Arabidopsis thalia	Arabidopsis thalia	E. coli colitose o	Streptococcus phen
ΔI	AAY33444	AAB19042	AAB19041	AAW41148	AAB19040	AAB19039	AAG42414	AAG42413	AAG42415	AAW88310	AAW51348
DB	20	21	21	19	21	21	21	21	21	20	19
Length	382	468	533	422	525	522	492	551	404	374	352
Query Match	28.9	14.5	13.9	13.8	13.8	13.6	13.3	13.3	12.3	6.8	5.8
Score	591.5	296.5	284	283	283	279.5	272	272	252	139	119
Result No.	1	7	m	4	ហ	٥	7	80	6	10	11
	Query Score Match Length DB ID	Ouery Score Match Length DB ID 591.5 28.9 382 20 AAY33444	Ouery Score Match Length DB ID 591.5 28.9 382 20 AAY33444 296.5 14.5 468 21 AAB19042	Ouery Score Match Length DB ID 591.5 28.9 382 20 AAY33444 296.5 14.5 468 21 AAB19042 284 13.9 533 21 AAB19041	Ouery Score Match Length DB ID 591.5 28.9 382 20 AAY33444 296.5 14.5 468 21 AAB19042 284 13.9 533 21 AAB19041 283 13.8 422 19 AAW41148	Ouery Score Match Length DB ID 591.5 28.9 382 20 AAY33444 296.5 14.5 468 21 AAB19042 284 13.9 533 21 AAB19041 283 13.8 525 21 AAB19040	Ouery Score Match Length DB ID 591.5 28.9 382 20 AAY33444 296.5 14.5 468 21 AAB19042 284 13.9 533 21 AAB19041 283 13.8 4.22 19 AAM41148 283 13.6 5.22 21 AAB19040 279.5 13.6 5.22 21 AAB19039	Ouery Score Match Length DB ID 591.5 28.9 382 20 AAY33444 296.5 14.5 468 21 AAB19042 284 13.9 533 21 AAB19041 283 13.8 422 19 AAW41148 279.5 13.6 522 21 AAB19039 272 13.3 492 21 AAG42414	Ouery Score Match Length DB ID 591.5 28.9 382 20 AAY33444 296.5 14.5 468 21 AAB19042 284 13.9 533 21 AAB19041 283 13.8 422 19 AAB1148 283 13.8 525 21 AAB19039 272 13.3 492 21 AAB19039 272 13.3 551 21 AAG42414	Ouery Score Match Length DB ID 591.5 28.9 382 20 AAY33444 296.5 14.5 468 21 AAB19042 284 13.9 533 21 AAB19041 283 13.8 525 21 AAB19040 279.5 13.6 522 21 AAB19039 272 13.3 492 21 AAB19039 272 13.3 492 21 AAB4141 252 12.3 404 21 AAG42415	Ouery Score Match Length DB ID 591.5 28.9 382 20 AAY33444 296.5 14.5 468 21 AAB19042 284 13.9 533 21 AAB19041 283 13.8 522 21 AAB19040 279.5 13.6 522 21 AAB19039 272 13.3 551 21 AAG42414 272 13.3 551 21 AAG42415 252 12.3 404 21 AAG42415 139 6.8 374 20 AAW88310

HIG-Bro	P-alucu	Human MSH2 protein	MSH2	ch repa	Uridine diphospho-	Streptococcus pneu	C. difficile toxin	Clostridium diffic	Japanese Black Pin	HUG-Br1, Homo sap	-1	PolC gene product	7		Ø	Arabidopsis thalia	Arabidopsis thalla	*	Helicobacter methi	DNA polymerase wit	Streptococcus pneu	Plasmodium falcipa	Streptococcus pneu	Human ORFX ORF1889	Staphylococcus epi	Lipid metabolism p	Arabidopsis thalla	H. pylori GHPO 479	•	Exophiala spinifer	Arabidopsis thalia	Streptococcus pneu	Arabidopsis thalia
AAR26154		AAR76063	AAR75411	AAW09034	AAW47126	AAY81719	AAR95011	AAW68388	AAR68893	AAR26153	AAW20999	AAY49070	AAB31934	AAG43513	AAG11789	AAG21988	AAG43514	AAW95039	AAW75910	AAW29322	AAY81750	AAB18217	AAW62736	AAB42125	AAW41602	AAB19190	AAG43515	AAW98305	AAW13729	AAY72635		17	AAG43120
13	21	16	16	18	19	21	17	19	14	13	18	20	22	21.	21	21	21	20	19	18	21	21	19	21	19	21	21	19	18	22	21	21	21
534	530	934	934	934	530	367	2366	2366	510	533	662	1435	1435	467	484	484	427	1151	648	1829	503	1802	350	1049	1092	1174	366	487	999	487	873	2120	397
5	5.2	٠		5.0	•	•	4.8	4	4.8	4.7	4.7	4.7	4.7	4.6	4.6	4.6	4.5	4.5	4.5	٠	4.4	4.4	4.3	4.3	4.3	4.3	4.3	4.3	4.3	4.3	4.3	4.3	4.2
109.5	106	102.5	102.5	102.5	102	101.5	98.5	98.5	86	96.5	96	95.5	95.5	- 95	94.5	94.5	92.5	92.5	92	92	90.5	06	68	68	68	68	88.5	88	88	87.5	87.5	87.5	87
12	13	14	15	16	17	18	19	20	21	22	23	24	25	26	27	28	29	30	31	32	33	34	35	36	37	38	33	40	41	42	43	44	45

## ALIGNMENTS

AAY33444 standard; Protein; 382 AA

AAY33444;

AAY33444 ID AAY3 XX· AC AAY3 XX

RESULT

Ē	13-DEC-1999 (first entry)
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DE	B. subtilis glycosyl transferase catalytic domain.
KW	Catalytic domain: glycosyl transferase: processive activity: determent
KW	oligosaccharide glycolipid: 3-oligoglucosyl-1,2-diacylglycerol:
ΚW	food emulsifier; polymer modifier; glycosyl transferase.
×	
SO	Bacillus subtilis.
XX	1.00
PN	DE19819958-A1.
×	
PD	30-SEP-1999.
XX	
PF	05-MAY-1998; 98DE-1019958.
XX	
PR	25-MAR-1998; 98DE-1013017.
XX	
PA	(GVSE-) GVS GES ERWERB & VERW LANDWIRTSCHAFTLICH.
ΡA	(BORS-) FORSCHUNGSZENTRUM BORSTEL ZENT MEDIZIN.
XX	
ΡΙ	Wolter FP, Jorasch P, Heinz E, Zaehringer U;
×	
DR	WPI; 1999-552364/47.
DR	N-PSDB; AAZ23386.
XX	
ΡŢ	New glycosyl transferase protein, useful for producing glycolipids -
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AAB19041
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                     This invention describes a novel protein (I) comprising identical or different catalytic domains of glycosyl transferases and which has processive activity (i.e. builds up oligosaccharide glycolipids by successive addition of glucose units). (I) can be used to produce 3-oligoglucosyl:1,2-diacylajveerols useful as food emulasifiers, polymer modifiers or detergents. This sequence represents a Bacillus subtilis glycosyl transferase catalytic domain which is used in the method of
                                                                                                                                                                                                                                                                                                                                              232
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                                                                                                                                                                                                                                                                                                                                                                                                                                                  FKYFRNMYKGFYYSRPDKLDKCFYK-----YYGL-NKLINLLIKE-KPDLILLTFPTPVM 117
                                                                                                                                                                                                                                                                                                  SVLTEQENINIPVATVMTDYRLHKNWITRYSTRYYVATKETKQDFIDVGIDPSTVKVTGI 177
                                                                                                                                                                                   Gaps
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4 nkrvliltanygnghyqvaktlyeqcvrlgfqhvtv--snlyqesnpivsevtqylylks 61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Amino acid sequence of monogalactosyl-diacylglycerol (MGDG) synthase
                                                                                                                                                                                                       5 NKKILLITGSFGNGHMQVTQSIVNQLNDMNLDHLSVIEHDLFMEAHPILTSICKKWYINS 64
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Monogalactosyl-diacylglycerol synthase; MGDG synthase; Toxoplasma; apicomplex parasite; herbicide; antiparasitic; Plasmodium; Eimeria; acquired immune deficiency syndrome; coccidiosis.
                                                                                                                                                                                                                                                                                                              PIDNKFET-----PINOKOWLIDNNLDPDKQTILMSAGAFGVSKGFDTMITDILAKSANA
                                                                                                                                                                                                                                                                                                                                                           QVVMICGKSKELKRSLTA-----KFKLTRMYLILGYTKHMNEWMASSQLMITKPGGIT
                                                                                                                                                                                   37;
                                                                                                                                                           Length 382;
                                                                                                                                                                                   Indels
                                                                                                                                                           DB 20;
                                                                                                                                                                                77; Mismatches 131;
                                                                                                                                                           28.9%; Score 591.5; DB 2 35.7%; Pred. No. 8.4e-48;
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Example 1; Page 7; 8pp; German.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 346 ISTMEQDKIKYATQTICRDLL 366
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                                                                                                    the invention.
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                                                                                                                                                                      Best Local Simi
Matches 136;
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synthase. MGGG is present in all plastids tested and is essential for cell survival, but is not present in other membrane structures, or in animal cells, and so represents a specific target. MGGG synthase or a plastid membrane isolated from plants is used to select and screen for specific inhibitors of MGDG synthase. These inhibitors are suitable as active agents against apicomplex parasites or as herbicides. The limbitors are used as antiparasitic agents, especially against plasmodium, Toxoplasma (particularly in patients with acquired immune deficiency syndrome) or Eimeria (coccidiosis in cattle or poultry), and
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Pred. No. 1.1e-19;
8; Mismatches 173
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Joyard J,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Example 2; Fig 2; 33pp; French.
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Block M,
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                                                                                                                                     WPI; 2000-602227/57.
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Marechal E,
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herbicides
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(first entry)

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Monogalactosyldiacylglycerol synthetase; MGDG; lipid production;
                                                                                                                                                                                                                                                                                                    New mono:galactosyl-di:acyl-glycerol synthase - useful
Increasing lipid production in transformed host
                                                   Monogalactosyldiacylglycerol synthetase sequence.
                                                                                                                                                                                                                                                                                                                                       Claim 1; Page 8; 13pp; Japanese.
                                                                                                                                                                                                                                      (KIRI ) KIRIN BREWERY KK.
                                                                                                                                                                                                                                                              WPI; 1998-138241/13.
N-PSDB; AAV12734.
                                                                                                                Cucumis sativus.
                                                                                                                                      JP10014579-A
                                                                                                                                                                                       02-JUL-1996;
                                                                                                                                                                                                              02-JUL-1996;
                           05-MAY-1998
                                                                                                                                                              20-JAN-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Matches 105;
                                                                                         cucumber.
   AAW41148
                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence
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Best Local 3
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                                                                                                                                                                                                                                                                     synthase. MCDG is present in all plastids tested and is essential for cell survival, but is not present in other membrane structures, or in animal cells, and so represents a specific target. MCDG synthase or a plastid membrane isolated from plants is used to select and screen for specific inhibitors of MCDG synthase. These inhibitors are suitable as active agents apicomplex parasites or as herbicides. The inhibitors are used as antiparasitic agents, especially against plasmodium, Toxoplasma (particularly in patients with acquired immune deficiency syndrome) or Eimeria (coccidiosis in cattle or poultry), and as herbicides.
                                                                                                                                                                                                                                                              present sequence represents a monogalactosyl-diacylglycerol (MGDG)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                314 sqikvyglpvrpsfvkpvrpkvelrrelgmdenl----pavllmgggegmgpieataral 369
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  66 KYFRN------MYKGFYYSRPDKL----DKCFYKYYGLNKLINLLIKEKPDLILLTFP- 113
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 114 ---TPVMSVLTEQFNINIPVATVMTDY-RLHKNWITPYSTRYYVATKETKQDFIDVGIDP 169
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                278 ITKPGGITITEGFARCIPMIFLNPAPGQELENAFYFEEKGFGKIADTPEEAIKIVASLTN 337
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 6 KKILIITGSFGNGHMQVTQSIVNQLNDMNLDHLSVIEHDLFMEAHPILTSICKKWYINSF 65
                                                                                                                                                                                   Use of monogalactosyl diacylglycerol synthase for identifying its specific inhibitors, potentially useful as antiparasitic agents and herbicides -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   254 mghvplrvlrskgllkkivfttvitdlstchptwfhklvtrcycpstevakragkaglet
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STVKVTGIPIDNKFETPINQKQWL----IDNNLDPDKQTILMSAGAFGV----SKGF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  219 DIMITDILAKSANAQVVMICGKSKELKRSLTA-KFKLTRMYLILGYTKHMNEWMASSQLM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            50;
                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 533;
                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 284; DB 21; Length 5
Pred. No. 2.1e-18;
5; Mismatches 185; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GNEQLINMISTMEQDKIKYATQ----TICRDLLDLI-GHSSQPQ 376
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                                                                                                                                     Douce
                                                                                                           (COMS ) COMMISSARIAT ENERGIE ATOMIQUE.
                                                                                                                                     Joyard J,
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                                                                                                                                                                                                                                   Example 2; Fig 2; 33pp; French.
                                                                                                                                                                                                                                                                                                                                                                                                                                                 13.9%;
25.5%;
                                                            17-MAR-2000; 2000WO-FR00658
                                                                                   99FR-0003434
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Matches 103; Conservative
                                                                                                                                     Block M,
                                                                                                                                                           WPI; 2000-602227/57.
                                                                                                                                                                                                                                                                                                                                                                                                                                                              Similarity
                                                                                                                                                                                                                                                                                                                                                                                                              533 AA;
           WO200056919-A1
                                                                                   19-MAR-1999;
                                                                                                                                     Marechal E,
                                   28-SEP-2000
                                                                                                                                                                                                                                                                                                                                                                                                               Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local (
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for, e.g

96JP-0172337 96JP-0172337

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13;
This sequence represents the monogalactosyldiacylglycerol synthase (MGDG) of the invention. This sequence was isolated from cucumber. MGDG may be used to increase lipid production in an organism.
                                                                                                                                                                                                                                                                                                                                                                   276 IMITKPGGITITEGFARCIPMIFLNPAPGQELENAFYFEEKGFGKIADTPEEAIKIVASL 335
                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               33 krvlilmsdtggghrasaeaikaafneefgnnyqvfitdlwtdhtp-----wpfnql
                                                                                                                                                                                                                                                                                                                                                                                                                                                       KKILIITGSFGNGHMQVTQSIVNQLNDMNLDHLSVIEHDLFMEAHPILTSICKKWYINSF
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STVKVTGIPIDNKFETPIN-----GKQMLIDNNLDPDKQTILMSAGAFGV----SKGF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DIMITDILAKSANAQVVMICGKSKELK -- - RSLTAKFKLTRMYLILGYTKHMNEWMASSQ
                                                                                                                                                                                                                                                                                                                                       KYFRN------MYKGFYYSRPDKL----DKCFYKYYGLNKLINLLIKEKPDLILLTFP-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               fgpk---adellimsqnalrlarpdavfkivhdlhelvkqrs-----fvpqys 421
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     336 TNGNEQLTNMISTMEQDKIKYATQ ----TICRDLLDLIGHSSQPQEIYGKVPLYA 386
                                                                                                                                                                                                         90;
                                                                                                                                                              Length 422;
                                                                                                                                                                                                         Indels
                                                                                                                                                          13.8%; Score 283; DB 19;
llarity 25.3%; Pred. No. 1.9e-18;
Conservative 65; Mismatches 185;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ¥.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAB19040 standard; protein; 525
                                                                                                                                                                               Similarity
                                                                                           422 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RESULT
AAB19040
ID AAB1
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AAW41148 standard; Protein; 422

RESULT
AAW41148
ID AAW4

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AAB19039;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       The present sequence represents a monogalactosyl-diacylglycerol (MGDG) synthase. MGDG is present in all plastids tested and is essential for cell survival, but is not present in other membrane structures, or in animal cells, and so represents a specific target. MGDG synthase or a plastid membrane isolated from plants is used to select and screen for specific inhibitors are suitable as active agents against apicomplex parasites or as herbicides. The inhibitors are used as antiparasitic agents, especially against plasmodium, Toxoplasma (particularly in patients with acquired immune deficiency syndrome) or Eimeria (coccidiosis in cattle or poultry), and as herbicides.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              66 KYFRN------MYKGFYYSRPDKL----DKCFYKYYGLNKLINLLIKEKPDLILLTFP- 113
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             247
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      275
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    364 skalydenhgepiggvlvicghnkklagrlrsidwkvpvg----vkgfvtkmeecmgacd 419
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LMITKPGGITITEGFARCIPMIFLNPAPGQELENAFYFEEKGFGKIADTPEEAIKIVASL 335
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                  Amino acid sequence of monogalactosyl-diacylglycerol (MGDG) synthase.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        6 KKILLIITGSFGNGHMQVTQSIVNQLNDMNLDHLSVIEHDLFMEAHPILTSICKKWYINSF 65
                                                                                                                                                                                                                                                                                                                                                                                                                                                       monogalactosyl diacylglycerol synthase for identifying its ic inhibitors, potentially useful as antiparasitic agents and
                                                                                                     Monogalactosyl-diacylglycerol synthase; MGDG synthase; Toxoplasma; apicomplex parasite; herbicide; antiparasitic; Plasmodium; Eimeria; acquired immune deficiency syndrome; coccidiosis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 | ::| || |: |: | || prsynflvkhgtlwkmtyyvtapkvihqsnfaatstfiarevakglmkyrpdiiisvhpl
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ---TPVMSVLTEQFNINIPVATVMTDY-RLHKNWITPYSTRYYVATKETKQDFIDVGIDP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               248 mqhvpirilrskgllnkivfttvvtdlstchptwfhklvtrcycpstevakraltaglqp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STVKVTGIPIDNKFETPIN-----OKQWLIDNNLDPDKQTILMSAGAFGV----SKGF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DTMITDILAKSANAQVVMICGKSKELK----RSLTAKFKLTRMYLILGYTKHMNEWMASSQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DB 21; Length 525;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      185;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    13.8%; Score 283; DB 21 25.3%; Pred. No. 2.6e-18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Pred. No. 2.6e; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                      Joyard J, Douce
                                                                                                                                                                                                                                                                                                                                                     (COMS ) COMMISSARIAT ENERGIE ATOMIQUE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      65;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Example 2; Fig 2; 33pp; French.
                                                                                                                                                                                                                                                                                17-MAR-2000; 2000WO-FR00658.
                                                                                                                                                                                                                                                                                                                   99FR-0003434
                                  (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                      Block M,
                                                                                                                                                                                                                                                                                                                                                                                                                      WPI; 2000-602227/57
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   525 AA;
                                                                                                                                                                           Cucumis sativus
                                                                                                                                                                                                            WO200056919-A1.
                                                                                                                                                                                                                                                                                                                   19-MAR-1999;
                                08-FEB-2001
                                                                                                                                                                                                                                                                                                                                                                                      Marechal E,
                                                                                                                                                                                                                                              28-SEP-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Best Local Sim
Matches 105;
                                                                                                                                                                                                                                                                                                                                                                                                                                                       Use of mono
specific in
herbicides
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence
AAB19040;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             188
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The present sequence represents a monogalactosyl-diacylglycerol (MGDG) synthase. MGDG is present in all plastids tested and is essential for cell survival, but is not present in other membrane structures, or in animal cells, and so represents a specific target. MGDG synthase or a plastid membrane isolated from plants is used to select and screen for specific inhibitors of MGDG synthase. These inhibitors are suitable as active agents against apicomplex parasites or as herbicides. The inhibitors are used as antiparasitic agents, especially against plasmodium, Toxoplasma (particularly in patients with acquired immune deficiency syndrome) or Eimeria (coccidiosis in cattle or poultry), and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              243 mghyplrilrgrgllekivfttvytdlstchptwfhklytrcycpsneyakratkaglgp 302
420 ciitkagpgtiaeamirglpiilndyjagqeagnvpyvvengcgkfskspkeianivakw 479
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Amino acid sequence of monogalactosyl-diacylglycerol (MGDG) synthase.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Monogalactosyl-diacylglycerol synthase; MGDG synthase; Toxoplasma; apicomplex parasite; herbicide; antiparasitic; Plasmodium; Eimeria; acquired immune deficiency syndrome; coccidiosis.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Use of monogalactosyl diacylglycerol synthase for identifying its specific inhibitors, potentially useful as antiparasitic agents a
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                                                                       336 INGNEQLINMISTMEQDKIKYATQ----TICRDLLDLIGHSSQPQEIYGKVPLYA
                                                                                                              : | || : : | || : | || || || 480 fgpk---adellimsgnalrlarpdavfkivhdlhelvkqrs-----fvpgys
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Pred. No. 5.5e-18;
64; Mismatches 191;
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24.5%;
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Protein identification; signal transduction pathway; metabolic pathway; hybridisation assay; genetic mapping; gene expression control; promoter; termination sequence.
             170 STVKVTGIPIDNKFETPINQKQWL-IDNNLDPDKQTILMSAGAFGV-----SKGFDTMI 222
                                  281
                                 223 TDILAKSANAQVVMICGKSKELKRSLTA-KFKLTRNYLILGYTKHMNEWMASSQLMITKP
                                                                                                                                                                                     Arabidopsis thaliana protein fragment SEQ ID NO: 52894
                                                                                         342 LTNMISTMEQDKIKYATQ----TICRDLLDLI 369
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                                                                                                                                          AAG42414 standard; Protein; 492 AA
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990S-0123180.
990S-0125788.
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16;
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                                                                                                                       56 IC---KKWYINSFKYFRN-----MYKGFYYSRPDKL----DKCFYKYYGLNKLINLLI 101
                                                                                                                                                   102 KEKPDLILLTFP----TPVMSVLTEQFNINIPVATVMTDY-RLHKNWITPYSTRYYVATK 156
                                                                                                                                                                                             157 ETKQDFIDVGIDPSTVKVTGIPIDNKFETPINQKQWL----IDNNLDPDKQTILMSAGA 211
                                                                                                                                                                                                                                      212 FGV-----SKGFDTMITDILAKSANAQVVMICGKSKELKRSLTA-KFKLTRMYLILGYT 264
                                                                                                                                                                                                                                                                                 265 KHMNEWMASSQLMITKPGGITITEGFARCIPMIFLNPAPGQELENAFYFEEKGFGKIADT 324
                                          Gaps
                                                               6 KKILIITGSFGNGHMQVTQSIVNQLN-DMNLDHLSVIEHDLFME------AHPILTS 55
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                     Length 492;
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                                          71; Mismatches 184;
                    13.3%; Score 272; DB 21; 24.9%; Pred. No. 2.6e-17;
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                    Query Match
Best Local Similarity 24.99
Matches 104; Conservative
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PR 05-WY-1999 903C-11240.

PR 11-WY-1999 903C-11248.

PR 11-WY-1999 903C-11248.

PR 11-WY-1999 903C-11248.

PR 11-WY-1999 903C-112418.

PR 11-WY-1999 903C-112418.

PR 11-WY-1999 903C-114218.

PR 21-WY-1999 903C-114218.

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27-AUG-1999; 27-AUG-1999; 15-SEP-1999; 16-SEP-1999; 20-SEP-1999; 22-SEP-1999; 23-SEP-1999; 99US-0158232. 99US-0158369. 99US-0159293.

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99US-0121825.
99US-0123180.
99US-0125788.
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                                                                                                                                                                                                                                                                                                                                                                   102 KEKPDLILLTFP----TPVMSVLTEQFNINIPVATVMTDY-RLHKNWITPYSTRYYVATK 156
                                                                                                                                                                                                                                                                                                                                                                                                                   | :||:|:
259 kygpdiiisvhplmqhvplrvlrskgllkkivfttvitdlstchptwfhklvtrcycpst 318
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  | : | : | : | : | | : | | evakraqkagletsqikvyglpvrpsfvkpvrpkvelrrelgmdenl----pavllmggg 374
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       |: :: :| | | ||::|||::||: |: :| |: |: 375 egmgpieataraladalydknlgeavggvliicgrnkklgsklssldwkip--vgvkgfi 432
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                                                                                                                                                                                                                                                                                                               ETKQDFIDVGIDPSTVKVTGIPIDNKFETPINQKQWL----IDNNLDPDKQTILMSAGA 211
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          265 KHMNEWMASSQLMITKPGGITITEGFARCIPMIFLNPAPGQELENAFYFEEKGFGKIADT 324
                                                                                                                                                                                                                                                                           Gaps
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                                                                                                                                                                                                                                                                                               6 KKILLIITGSFGNGHMQVTQSIVNQLN-DMNLDHLSVIEHDLFME------AHPILTS 55
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       325 PEEAIKIVASLINGNEQLINMISTMEQDKIKYATQ----TICRDLLDLI-GHSSQPQ 376
                                                                                                                                                                                                                                                                         58;
                                                                                                                                                                                                                                              13.3%; Score 272; DB 21; Length 551; 24.9%; Pred. No. 3.1e-17; ive 71; Mismatches 184; Indels 58
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Arabidopsis thaliana protein fragment SEQ ID NO: 52895.
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Matches 104; Conservative
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63 NSFKYFRN-----MYKGFYYSRPDKL----DKCFYKYYGLNKLINLLIKEKPDLILLT 111
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62 nqlprsynflvkhgtlwkmtyygtsprivhgsnfaatstfiareiagglmkyqpdinisv 121
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  167 IDPSTVKVTGIPIDNKFETPINQKOWL----IDNNLDPDKQTILMSAGAFGV----S
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29-SEP-1999, 04-0c7-1999, 06-0c7-1999, 06-0c7-1999, 13-0c7-1999, 13-0c7-1999, 13-0c7-1999, 14-0c7-1999, 14-0c7-1999, 14-0c7-1999, 13-0c7-1999, 13-0c
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AAW88310 standard; Protein; 374 AA.

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277 MITKPG----GITITEGFARCIPMIFLNPAPGQE---
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                                                                                                                                                               O antigen; Olll antigen; wbdM gene; colitose transferase; glucose transferase; diarrhoea; haemorrhagic colitis; diagnosis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Nucleic acid molecules specific for bacterial polysaccharide antigens - useful for detecting specific strains in, e.g. food,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      86;
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20.9%; Pred. No. 7.3e-05;
iive 69; Mismatches 163;
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Best Local Similarity 20.9
Matches 84; Conservative
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AAW88310;
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19;
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                                                                                                                                                                                                                                         Streptococcus pneumoniae; stem peptide biosynthesis; murg; inhibitor; infection; antibiotic resistant; microorganism; bacteria; cell wall biosynthesis.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TFPTPVMSVLTEQFNINIPVATVMTDYR--LHKNWITPYSTRYYVATKETKQDFIDVGID 168
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          nbinant Streptococcus pneumoniae MurG protein encoded by nucleic expressed in host cells - useful in screening for inhibitors of protein and stem peptide biosynthesis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      7 KILIITGSFGNGHMQVTQSI------VNQLND-MNLDHLSVIEHDLFMEAHPILTS 55
                                                                                                                                                                                                                    Streptococcus pneumoniae stem peptide biosynthetic murG protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 352;
270 fvlssewegfglvvaeamacerpvvatdsggvkevvgphndvipvsnhillae-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Indels
                                               323 DT---PEEAIKIVASLTN----GNEQLTNMISTMEQDKIKYA 357
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Mismatches 155;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DB 19;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          0.0053;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           5.8%; Score 119;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Skatrud PL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Claim 1; Page 15-16; 20pp; English.
                                                                                                                                   Ą
                                                                                                                                AAW51348 standard; Protein; 352
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        80;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     beta-lactam resistant bacteria
                                                                                                                                                                                                                                                                                                                                                                                                97EP-0309247.
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                                                                                                                                                                                          (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Conservative
                                                                                                                                                                                                                                                                                                            Streptococcus pneumoniae.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Hoskins JA, Peery RB,
                                                                                                                                                                                                                                                                                                                                                                                                                                                          (ELIL ) LILLY & CO ELI.
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Best Local Similarity
...... 79; Conserve
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WPI; 1998-263289/24.
N-PSDB; AAV07310.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                352 AA;
                                                                                                                                                                                                                                                                                                                                                                                                18-NOV-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                             19-NOV-1996;
                                                                                                                                                                                          03-SEP-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Recombinant
                                                                                                                                                                                                                                                                                                                                      EP843012-A2
                                                                                                                                                                                                                                                                                                                                                                   20-MAY-1998
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STVKVTGIP---IDNKFETPINQKQWLIDNNLDPDKQTILMSAGAFGVSKGFDTMITD--

97

62 INSFKYFRNMYKGFYYSRPDKLDKCFYKYYGLNKLINLLIKEKPDLI---

 In contrast, they have unique 5' ends

¥

534

Sequence

SXS

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Two human liver bilirubin UDP-glucuronosyltransferase cDNAs have been isolated. They are referred to as HUGB1 (AAQ27369) and HUGB12 (AAQ27370) (Ritter, et al., J. Biol. Chem. 266:1043-1047 (1991)) and, upon expression individually in COS-1 calls, encode isoforms that catalyse the formation of the two bilirubin monoglucuronides and
                   210 kelteryniinltgdsslnelsgnlfrvdyvtdlygpl-----meladvvvtrgga 260
                                                                                                     284 ITITEGFA----RCIPMIFLNPAPGQELENAFYFEEKGFGKIADTPEEAIKIVASLTNGN 339
PSTVKVTGIPIDNKFETPINQKQWLID--NNLDPDKQTILMSAGAFGVSKGFDTMITDIL 226
                                                                                                                     AK-SANAQVVMICGKS--KELKRSLTAKFKLTRMYLILGYTKHMNEWMASSQLMITKPGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /note- "predicted Asn-linked glycosylation site" 282..285
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              the diglucuronide.
The cDNAs contain identical 3' emis (1469 bp in length) to each other and to that of the human phenol transferse cDNA, HLUGPl (Harding et al., Proc. Natl. Aca. Sci. USA 85:8281 (1988)).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Isolated gene locus UGT1, DNA segments and diagnostic probes for diagnosing Gilbert's disease and Crigler-Najjar syndrome types I and II
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /note= "residues encoded by TGCCAACGGGAAG !"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          membrane-anchoring peptide"
                                                                                                                                                                                                                                                                                                                                                                                                                                           /note= "putative membrane-insertion signal"
                                                                                                                                                                                                                                                                                                                                                      Bilirubin; UDP-glucuronosyltransferase; HUGBr1; HUGBr2; monoglucuronide; diglucuronide.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (USSH ) US DEPT HEALTH & HUMAN SERVICE.
                                                                                                                                                                       EQLTNMISTMEQDKIKYATQTICRDLLD 367
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Disclosure; Fig 9A-I; 99pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                       Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                 492..508 /note= "putative m. 348
                                                                                                                                                                                                                                                  534
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                                                                                                                                                                                                                                                AAR26154 standard; Protein;
                                                                                                                                                                                                                                                                                                    (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Ritter JK;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WPI; 1992-284593/34.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          N-PSDB; AAQ27369
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Misc-difference
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Modified-site
                                                                                                                                                                                                                                                                                                                                                                                              Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     10-JAN-1992;
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                                                                                                                                                                                                                                                                          AAR26154;
                                                                                                                                                                                                                                                                                                                              HUG-Br2
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Region
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 169
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12;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Novel human UDP-glucuronosyltransferase sequence, polymorphisms for genotyping individuals to predict rate of metabolism of substrates and for identifying potential drug interactions
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              UDP-glucuronosyltransferase 2815; UGT2815; polymorphism; metabolism; drug interaction; detect; human; single nucleotide polymorphism; SNPs.
                                                                                                                                                                                                                              297 ----asgehgivvfslesmvseipekkama----iadalgkipqtvlwrytgtrpsnlan 348
                                                                93 LNKLINLLIKEKPOLILLTFPTPVMSVLTEQFNINIPVATVMTDYRLHKNWITPYSTRYY 152
                                                                                                                               153 VATKETKODFI---DVGIDPSTVKVTGI-----PIDNKFETPINQKQWLIDNNLDPDKQ 203
                                                                                                                                                                                                                                                                                               349 nt-ilvkwlpqndllghpmtrafithagshgvyesicngvpmvmm-plfgdqmdnakrme 406
                                                                                                                                                                                                 204 TILMSAGAFG-VSKGFDTMITDILAKSANAQVVMICGKSKELKRSLTAKFKLTRMYLILG
                                                                                                                                                                                                                                                               263 YTKHMNEWMASSQLM-----ITKPGGITITEGFARCIPMIFLNPAPGQELENAFYFE
                                 65;
 Length 534;
                                                                                 Human UDP-glucuronosyltransferase 2B15 amino acid sequence.
                                  Indels
                                                                                                                                                                                                                                                                                                                                                       407 tkgagvtlnvlemtsedlenagkavindksykenimrlsslhkdr 451
                                                                                                                                                                                                                                                                                                                                315 EKGFGKIAD ----TPEEAIKIVASLINGNEQLINM--ISTMEQDK 353
Score 109.5; DB 13;
Pred. No. 0.078;
54; Mismatches 108;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Riedy M;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Disclosure; Page 59-60; 72pp; English.
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5.3%;
ilarity 20.4%;
Conservative 5
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                 Similarity
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 Query Match
Best Local Simi
Matches 58;
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26-MAY-1995.

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                                                                                                                                                                                                                                                24;
comprise human UGT2B sequence polymorphisms (see AAZ95051-Z95110). Probes which detect the UGT2B locus polymorphisms can be used to detect altered UGT2B metabolism of a substrate in an individual. The nucleic acid molecules comprising a human UGT2B sequence polymorphism can be used in sereening assays for genotyping individuals, also to predict their rate of metabolism of UGT2B substrate, potential drug-drug interactions and adverse side effects. The polymorphisms can be used as single nucleotide polymorphisms (SNRs) for detecting genetic linkage related to phenotypic variation in activity or expression of UGT2B protein. The polymorphism containing nucleic acid molecules may also be used for generating genetically modified non-human animals and for obtaining site specific gene modification in cell lines.
                                                                                                                                                                                                                                                                                                                                                                                             138 RLH----KN-----WITPYSTRYYVATKETKQDFIDVGIDPSTVKVTGIPIDNKFE 184
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        250 tmgkaemwlirtywdfefprpflpnvdfvgglhckpakplpkemeefvgssgengivvfs 309
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 216 KGFDTMITDILAKSANAQVVMICGKSKELKRSLTAKFKLTRMYLILGYTKHMNEWMASSQ 275
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         310 lg--smisnmseesan----miasalaqipqkvlwrfd-gkkpntlgsntrlykwlpqnd 362
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     328 AIKIVASLTNGNEQLTNMISTMEQDKI-KYATQTICRDLLDLIGHSSQPQEIYGKVPLYA 386
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  61 YINSF-----KYFRNMYKGFYYSRPDKLDKCFYKYYG------LNKLINLLIKE-K 104
                                                                                                                                                                                                                                                                                                                                                                             -----NIPVA-TVMTDY 137
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   276 LM------ITKPGGITITEGFARCIPMIFLNPAPGQELENAFYFEEKGFGKIADTPEE 327
                                                                                                                                                                                                                                                                          1 MVTQNKKILLITGSFGNGHMQVTQSIVNQLNDMNLDHLSVIEHDLFMEAHPILTSICKKW 60
                                                                                                                                                                                                                                                                                       --PDKQTILMSAGAFGV---S
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Mismatch repair; MSH2; primer; identification; defect; alteration;
                                                                                                                                                                                                                                                Indels 154;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Human MSH2 protein, homologue of the E.coli muts gene product.
                                                                                                                                                                                                                       Length 530;
                                                                                                                                                                                                                     Score 106; DB 21;
Pred. No. 0.16;
8; Mismatches 160;
                                                                                                                                                                                                                                                                                                                                                                             105 PDLILLTFPTPVMSVLTEQFNI--------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAR76063 standard; Protein; 934 AA.
                                                                                                                                                                                                       5.2%; Scor.
7 19.2%; Pred
7 78; }
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                                                                                                                                                                                                                                                Conservative
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                                                                                                                                                                                                                     Query Match
Best Local Similarity
                                                                                                                                                                                 530 AA;
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                                                                                                                                                                                                                                                93;
                                                                                                                                                                                  Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAR76063;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  63 NSFKYFRNMYKGFYYSRPDKLDKCFYKYYGLNKLINLL-IKEKPD-----LILLTFFTFV 116
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 539 fstvdigkngvkftns----klts--lneeytknkteyeeaqdaivkei--vnissgyv 589
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        117 MSVLTE--QFNINIPVATVMTDXRLHKNWITPXSTRYYVATKETKQDFIDVGIDPSTVKV 174
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TGI--PIDNKFE-TPINQKQWLIDNNLDPDKQTILMSAGAFGVSKGFDTMITDILAKSAN 231
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              232 AQVVMICGKSKELKRSLTAKFKLTRMYLILGYTKHMNEWMASSQLMITKPGGITITEGFA 291
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GHMOVTOSIVNOLNDMNL--DHLSVIE------HDLFMEAHPILTSICKKWYI 62
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAQ93901 is the human mismatch repair pathway gene MSH2. Defects or alterations in such a gene result in the accumulation of unstable repeated DNA sequences, a feature of a number of different cancers. The identification of a defect in the mismatch repair pathway can be diagnostic of a predisposition to cancer and prognostic for a particular mammalian cancer e.g colorectal, ovarian, endometrial (uterine), renal, bladder, skin, rectal and bowel. The nucleotide the account of the mismatch of the hMSH2 gene may also be used for
                                                                                                                                                                                                                                                                                                                                                                                    - used in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ggrlvngwikgplmdknrieerlnlveafvedaelrgtlgedl-1rrfpdlnrlakk---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             41 tdlrsdfskfqemiettldmdqvenheflvkp------sfdpnlsel
                                                                                                                                                                                                                                                                                                                                                                                    Determining alteration in human mismatch repair pathways - used the diagnosis, prognosis and therapy of cancers and in screening
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       93;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 934;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    45; Mismatches 131; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         292 RCIPMIFLNPAPGQELENAFYFE---------EKGFGKI 321
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DB 16;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    5.0%; Score 102.5; D 22.3%; Pred. No. 0.81;
                                                                                                                                                                UNIV VERMONT & STATE AGRIC COLLEGE. DANA FARBER CANCER INST.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Claim 27; Page 159-163; 256pp; English.
                                                                                                                                                                                                                                                  Reenan RAG;
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                                                  94US-0259310.
93US-0154792.
93US-0163449.
  94WO-US13385
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                                                                                                                                                                                                                                                                                                  WPI; 1995-200377/26.
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Best Local Similarity
Matches 77; Conserve
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     934 AA;
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17-NOV-1994;
                                                                              17-NOV-1993;
07-DEC-1993;
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                                                                                                                                                                                                                                               Fishel R,
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17;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                117 MSVLTE--QFNINIPVATVMTDYRLHKNWITPYSTRYYVATKETKQDFIDVGIDPSTVKV 174
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         441 tdlrsdfskfgemiettldmdgvenheflvkp-------sfdpnlsel 481
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   175 TGI--PIDNKFE-TPINQKQWLIDNNLDPDKQTILMSAGAFGVSKGFDTMITDILAKSAN 231
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ---HDLFMEAHPILTSICKKWYI 62
                                                                                                                                                                                                                                                                                                New cDNA from human MSH2 gene encoding DNA mismatch repair enzyme tis mutants causing hereditary non-polyposis colorectal cancer and derived proteins useful in cancer prevention or treatment and for diagnosis and screening.
                                                                                                                                                                                                                                                                                                                                                                                          cDNA from human colon cancer cells was amplified using primers previously used to isolate the yeast MSH2 gene from homology with Muts. The insert in isolated clone pNP-23 was used to screen cDNA libraries, and positive clones were used in a chromosome walking procedure to identify the entire coding sequence (given in AAQ87269) of the human MSH2 gene.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              93;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 934;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              5.0%; Score 102.5; DB 16; Length 22.3%; Pred. No. 0.81; tive 45; Mismatches 131; Indels
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                                                                                                                                                                                                                                 Vogelstein B;
                                       hereditary non-polyposis colorectal cancer.
                           mutator gene; DNA mismatch repair;
                                                                                                                                                                                                                                                                                                                                                                Disclosure; Page 37-38; 60pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      18 GHMQVTQSIVNQLNDMNL--DHLSVIE:
                                                                                                                                                                                                                                 Kinzler KW,
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Best Local Similarity 22.38
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N-PSDB; AAQ87269.
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                                                                   Homo sapiens
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                                                                                                                      08-JUN-1995
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2048 1 MVTQNKKILIITGSFGNGHM.....SSQPQEIYGKVPLYARFFVK 391 Perfect score:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table: Sedneuce:

219241 seqs, 76174552 residues Searched:

219241 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

PIR\_68:\*
1: pirl:\*
2: pir2:\*
3: pir3:\*
4: pir4:\* Database

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

	Description	cell wall synthesi	probable monogalac	probable cell wall	1,2-diacylglycerol	probable 1, 2-diacy		conserved hypothet	hypothetical prote	σ	NUP133 protein - y	UDP-N-acetylqlucos	phospho-N-acetylmu	SRPM54 protein - M	hypothetical prote	transferase, pepti	udp-n-acetylqlucos	peptidoglycan synt	hypothetical prote	н	hypothetical prote	lipopolysaccharide	phospho-N-acetylmu	qlucuronosyltransf	hypothetical prote		hypothetical prote	phosphorylation-ac	UDP-N-acetylqlucos	hypothetical prote
SUMMARIES	OI.	C69935	C84499	F75439	T52269	T05092	T10478	в69860	E83894	F70195	S38160	E83970	C70401	S35481	T44333	C6466	G71852	E86823	F64456	S70962	A71655	E70156	JC1275	A35343	D84955	C72590	T28722	260880	B72402	A86065
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	Score	591.5	309	299	296.5	284	283	245	230	136	127.5	124	123.5	122	121	117.5	116.5	116.5	115.5	113.5	113	112.5	111.5	109.5	109	108.5	108.5	106	106	106
	Result No.	-	7	e	4	5	9	7	8	6	10	11	12	13	14	15	16	17	18	19	50	21	22	23	24	25	<b>5</b> 6	27	28	53

	qlucuronosyltransf	hypothetical prote	hypothetical prote	qlucuronosyltransf	toxin, nontoxic co	botulinum neurotox	spore coat polysac	hypothetical prote	DNA mismatch repai	bacteriophage N4 a	hypothetical prote	mannosvltransferas	type III restricti	qlucuronosyltransf	reverse dyrase - S	hypothetical prote	
	A48633	T27589	T43990	A24600	JQ1467	S46430	E64432	T19944	I64819	E65182	F40511	F70346	A64691	157961	A47445	T19365	
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	530	533	1082	529	1196	1196	484	534	934	389	398	368	474	535	1248	530	
	5.2	5.2	5.2	5.1	5.1	5.1	5.1	5.0	5.0	2.0	5.0	5.0	5.0	5.0	5.0	4.9	
=	106	106	106	104.5	104	104	103.5	102.5	102.5	102	102	101.5	101.5	101.5	101.5	101	
	30	31	32	33	34	32	36	37	38	39	40	41	42	43	44	45	

## ALIGNMENTS

	RESULT 1
	C69935
	cell wall synthesis homolog ypfP - Bacillus subtilis
	C;Species: Bacillus subtilis
	C;Date: 05;Dec-1997 #sequence_revision 05-Dec-1997 #text_change 15-Oct-1999
	C; Accession: C69935
	R; Kunst, F; Ogasawara, N.; Moszer, I.; Albertini, A.M.; Alloni, G.; Azevedo, V.; Ber
	C.; Bron, S.; Brouillet, S.; Bruschi, C.V.; Caldwell, B.; Capuano, V.; Carter, N.M.;
	A.; Ehrlich, S.D.; Emmerson, P.T.; Entian, K.D.; Errington, J.; Fabret, C.; Ferrari
	Nature 390, 249-256, 1997
	A; Authors: Foulger, D.; Fritz, C.; Fujita, M.; Fujita, Y.; Fuma, S.; Galizzi, A.; Gal
	iech, J.; Harwood, C.R.; Henaut, A.; Hilbert, H.; Holsappel, S.; Hosono, S.; Hullo, M
	Koetter, P.; Koningstein, G.; Krogh, S.; Kumano, M.; Kurita, K.; Lapidus, A.; Lardino
	A; Authors: Lauber, J.; Lazarevic, V.; Lee, S.M.; Levine, A.; Liu, H.; Masuda, S.; Mau
	y, M.; Ogawa, K.; Ogiwara, A.; Oudega, B.; Park, S.H.; Parro, V.; Pohl, T.M.; Portete
	Rieger, M.; Rivolta, C.; Rocha, E.; Roche, B.; Rose, M.; Sadale, Y.; Sato, T.; Scanl
	A; Authors: Schleich, S.; Schroeter, R.; Scoffone, F.; Sekiquchi, J.; Sekowska, A.; Se
	akeuchi, M.; Tamakoshi, A.; Tanaka, T.; Terpstra, P.; Tognoni, A.; Tosato, V.; Uchiya
	T.; Winters, P.; Wipat, A.; Yamamoto, H.; Yamane, K.; Yasumoto, K.; Yata, K.; Yoshida
	A; Authors:   Yoshikawa, H.F.; Zumstein, E.; Yoshikawa, H.; Danchin, A.
_	A; Title: The complete genome sequence of the Gram-positive bacterium Bacillus subtili
	A; Reference number: A69580; MUID: 98044033

A; wererence number: A69580; MUID: 98044033
A; Accession: C69935
A; Status: preliminary; nucleic acid sequence not shown; translation not shown
A; Molecule type: DNA
A; Residues: 1-382 <KUN>
A; Cestion: C69534478; PIDN: CAB14110.1; PID: e11836
A; Experimental source: strain 168
C; Genetics:
A; Gene: ypfp

10; Gaps Indels 37; Length 382; Ouery Match 28.9%; Score 591.5; DB 2; Best Local Similarity 35.7%; Pred. No. 3.3e-37; Matches 136; Conservative 77; Mismatches 131;

4		7	
NKKILIITGSFGNGHMQVTQSIVNQLNDMNLDHLSVIEHDLFMEAHPILTSICKKWYINS 64		NKRVLILTANYGNGHVQVAKTLYEQCVRLGFQHVTV SNLYQESNPIVSEVTQYLYLKS 61	
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118 SVLTEQFNINIPVATVMTDYRLHKNWITPYSTRYYVATKETKODFIDVGIDPSTVKVTGI 177 δ 셤 ò

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178 PIDNKFET-----PINGKQWLIDNNLDPDKQTILMSAGAFGVSKGFDTMITDILAKSANA 232 δ

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Gaps

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A)Cross-references: GB:AE001958; GB:AE000513; NID:g6458805; PIDN:AAF10649.1; PID:g645 A; Experimental source: strain R1 C; Genetics: A; Genetics: A;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1,2-diacylglycerol 3-beta-galactosyltransferase (EC 2.4.1.46) [imported] - Arabidopsi N;Alternate names: monogalactosyldiacylglycerol synthase C;Species: Arabidopsis thaliana (mouse-ear cress) C;Species: 20-Oct-2000 #sequence_revision 20-Oct-2000 #text_change 20-Oct-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          C,Accession: T52269
R;Awai, K.; Shimojima, M.; Masuda, T.; Takamiya, K.I.; Ohta, H.
submitted to the EMBL Data Library, July 1998
A;Description: cDNA cloning of an Arabidopsis monogalactosyldiacylglycerol synthase
A;Reference number: Z26011
                 Riwhite, O.; Eisen, J.A.; Heidelberg, J.F.; Hickey, E.K.; Peterson, J.D.; Dodson, M.; Shen, M.; Vamathevan, J.J.; Lam, P.; McDonald, L.; Utterback, T.; Zalewski, S.; Smith, H.O.; Venter, J.C.; Fraser, C.M.
Science 26(, 1571-1577, 1999)
A;Title Genome sequence of the radioresistant bacterium Deinococcus radiodurans FA;Reference number: A75250; MUID: 20036896
A;Status: preliminary
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-411 <WHI>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              121 TEQENINIPVATVMTDYRLHKNWITPYSTRYYVATKETKQDFIDVGIDPSTVKVTGIPID 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NKFETPINQKQWLI-----DNNLDPDKQTILMSAGAFGVSKGFDTMITDILAKSAN---
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    29 RALFMSVSLGAGHDQAQQAVKQAFAERGVELLGA-EHDSVEYLSTFERSFTVDLYEFELR
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          14.6%; Score 299; DB 2; L 25.3%; Pred. No. 4.7e-15; iive 63; Mismatches 153;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  14.5%; Score 296.5; DB 2; ilarity 25.4%; Pred. No. 8.7e-15; Conservative 78; Mismatches 173;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A;Gene: mgd
C;Keywords: glycosyltransferase; hexosyltransferase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A;Status: preliminary; translated from GB/EMBL/DDBJ
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A; Experimental source: cultivar Columbia
C; Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EGFARCIPMIFLNPAPGQELENAFYFEEKGFG 319
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Best Local Similarity 25.3%
Matches 84; Conservative
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A; Residues: 1-468 < AWA>
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R; Lin, X.; Kaul, S; Rounsley, S.D.; Shea, T.P.; Benito, M.I.; Town, C.D.; Fujii, C.Y.; M.; Koo, H.; Moffat, K.S.; Cronin, L.A.; Shen, M.; Vanaken, S.E.; Umayam, L.; Tallon, L. euss, D.; Nierman, W.C.; White, O.; Elsen, J.A.; Salzberg, S.L.; Fraser, C.M.; Venter, Nature 402, 761-768, 1999
A; Title: Sequence and analysis of chromosome 2 of the plant Arabidopsis thaliana. A; Reference number: A84420; MUID:20083487
A; Accession: C84499
A; Accession: C84499
A; Accession: C84499
A; Residues: preliminary
A; Residues: Jr464 cSTO>
A; Cross-references: GB:AE002093; NID:94734000; PIDN:AAD28678.1; GSPDB:GN00139
C; Genetics: A; Genetics: 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         probable monogalactosyldiacylglycerol synthase [imported] - Arabidopsis thaliana C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 02-Feb-2001 #sequence_revision 02-Feb-2001 #text_change 02-Feb-2001 C;Accession: C84499
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               16;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         168
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      232 QVVVVCGKNTALKESLSALEAENGDKLK-----VLGIVERIDELFRITDCMITKPGGIT 285
                                                                                                                                                                    ITEGFARCIPMIFLNPAPGQELENAFYFEEKGFGKIADTPEEAIKIVASLTNGNEQLINM 345
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   6 KKILIITGSFGNGHMQVTQSIVNQLNDMNLDHLSVIEHDLFMEAHPILTSICKKWYINSF
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25.4%; Pred. No. 9.7e-16;
Live 83; Mismatches 178;
                                                                                                                                                                                                                                                                                                                                              346 ISTMEQDKIKYATQTICRDLL 366
                                                                                                                                                                                                                                                                                                                                                                                               346 KKNIKDLHLANSSEVILEDIL 366
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C; Accession: T16478
R; Shimojima, M.; Ohta, H.; Iwamatsu, A.; Masuda, T.; Shiol, Y.; Takamiya, K.
Proc. Natl. Acad. Sci. U.S.A. 94, 333-337, 1997
A; Title: Cloning of the gene for monogalactosyldiacylglycerol synthase and its evolut A; Reference number: Z17042; MUID:97144442
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                                                                                                                                                                                                                                                             probable 1,2-diacylglycerol 3-beta-galactosyltransferase (EC 2.4.1.46) precursor, N.Alternate names: monogalactosyldiacylglycerol synthase C; Species: Cucumis sativus (cucumber) C; Species: Cucumis sativus (cucumber) C; Date: 16-Jul-1999 #sequence_revision 16-Jul-1999 #text_change 21-Jul-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              13;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A;Cross-references: EMBL:U62622; NID:91805253; PIDN:AAC49624.1; PID:91805254 A;Experimental source: cv. Aonagajibai; 5 day old seedlings C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A; Description: catalyzes the formation of monogalactosyldiacylglycerol, a m A; Pethway: membrane lipid biosynthesis
C; Reywords: chicroplast; glycosyltransferase; hexosyltransferase
F; 1:103/Domain: transit peptide (chloroplast) #status predicted C;Reywords: 1,2-diacylglycerol 3-beta-galactosyltransferase #status
                                                                    428 ITKAGPGTIAEAMIRGLPIILNGYIAGQEAGNVPYVVENGCGKFSKSPKEISKIVADWFG 487
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          247
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               114 ---TPVMSVLTEQFNINIPVATVMTDY-RLHKNWITPYSTRYYVATKETKQDFIDVGIDP 169
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            308_SKLKVFGLPVRPSFVKPIRPKIELRKELGMDENL----PAVLLMGGGEGMGPIEATAKAL 363
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         370 ADALYDKNLGEAVGQVLIICGRNKKLQSKLSSLDWKIP--VQVKGFITKMEECMGACDCI 427
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         136 KRVLIIMSDTGGGHRASAEAIKAAFNEEFGNNYQVFITDLWTDHTP------WPFNQL 187
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               276 LMITKPGGITITEGFARCIPMIFLNPAPGQELENAFYFEEKGFGKIADTPEEAIKIVASL 335
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRSYNFLVKHGTLWKMTYYVTAPKVIHQSNFAATSTFIAREVAKGLMKYRPDIIISVHPL
                                        ITKPGGITITEGFARCIPMIFLNPAPGQELENAFYFEEKGFGKIADTPEEAIKIVASLTN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           170 STVKVTGIPIDNKFETPIN----QKQWLIDNNLDPDKQTILMSAGAFGV----SKGF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     66 KYFRN------MYKGFYYSRPDKL----DKCFYKYYGLNKLINLLIKEKPDLILLTFP-
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          480 FGPK---ADELLIMSQNALRLARPDAVFKIVHDLHELVKQRS------FVPQYS 524
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                                                                                                                                                 ---PASKELEIMSQNALRLAKPEAVFKIVHDMHELVRKKNSLPQ 528
                                                                                                                        338 GNEQLTNMISTMEQDKIKYATQ----TICRDLLDLI-GHSSQPQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 13.8%; Score 283; DB 2; L ilarity 25.3%; Pred. No. 1.1e-13; Conservative 65; Mismatches 185;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A;Status: preliminary; translâted from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 1-525 <SHI>
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Best Local Similarity
Matches 105, Conserva
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C; Function:
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                                        118
                                                                                                                                                                                                     237
                                                                                                                                                                                                                                       167 IDPSTVKVTGIPIDNKFETPINQKQWL-IDNNLDPDKQTILMSAGAFGV-----SKGFD 219
                                                                                                                                                                                                                                                                     220 TMITDILAKSANAQVVMICGKSKELKRSLTA-KFKLTRMYLILGYTKHMNEWMASSQLMI 278
                                                                                                                                                                                                                                                                                                                                                                  355
                                                                                                                                                                                                                                                                                                                                                                                                          334
                                                                                                                                                                                                                                                                                                                                                                                                                                ----SFKYF---RNMYK-GFYYSRPDKLDKCFY----KYYGLNKLINLLIKEKPDLILLT 111
                                                                                                      112 FP----TPVMSVLTEQFNINIPVATVMTDYR-LHKNWITPYSTRYYVATKETKQDFIDVG 166
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    142 KKVLILMSDTGGGHRASAEAIRAAFNQEFGDEYOVFITDLWTDHTP------WPFNQL 193
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           66 KYFRN------MYKGFYYSRPDKL----DKCFYKYYGLNKLINLLIKEKPDLILLTFP- 113
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                114 ---TPVMSVLTEQFNINIPVATVMTDY-RLHKNWITPYSTRYYVATKETKQDFIDVGIDP 169
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                                        ----YTGWPLN
                                                                                                                                                                                              178 HPLMOHIPLWYLKWOELOKRVLFVTVITDLNTCHPTWFHPGVNRCYCPSQEVAKRALFDG
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                                                                                                                                                                                                                                                                                                                                            279 TKPGGITITEGFARCIPMIFLNPAPGQELENAFYFEEKGFGKIADTPEEAIKIV----AS
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25.5%; Pred. No. 9.2e-14;
Live 66; Mismatches 185; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A;Cross-references: EMBL:AL031004
A;Experimental source: cultivar Columbia; BAC clone F28M20
C;Genetics:
                                    RTKNVLILMSDTGGGHRASAEAIRDAFKIEFGDKYRVIVKDVWKE-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A; Map position: 4
A:Introns: 175/3; 233/2; 287/2; 334/3; 409/3; 430/3; A; Note: F28420.30
C; Keywords: glycosyltransferase; hexosyltransferase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               335 LINGNEQLINMISTMEQDKIKYATQTICRDLLDL 368
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match 13.99
Best Local Similarity 25.55
Matches 103; Conservative
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1-533 <BEV>
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A; Residues: 1-533
                                    67
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A;Accession: E83894
A;Status: preliminary
A;Acatus: preliminary
A;Molecule type: DNA
A;Residues: 1-374 <STO>
A;Cross-references: GB:AP001513; GB:BA000004; NID:g10174345; PIDN:BAB05676.1; GSPDB:G
A;Cross-references: strain C-125
C;Genetics: A;Gene: BH1957
                                                                                                                                                                                                                                                                                         11.2%;
21.8%;
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Best Local Similarity 21.25
Matches 86; Conservative
                                                                                                                                                                                                                                                                                                                                                83; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     298 FLNPAPGOELENAFY---
                                                                                                                                                                                                                                                                                                                   Local Similarity
                                                                                                                                                                                                                                                                                         Query Match
Best Local Si
Matches 83;
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                                                                                            C; Accession: B69860
R; Kunst, F.; Ogasawara, N.; Moszer, I.; Albertini, A.M.; Alloni, G.; Azevedo, V.; Berter
C; Accession: B69860
R; Kunst, F.; Ogasawara, N.; Moszer, I.; Albertini, A.M.; Alloni, G.; Azevedo, V.; Berter
C.; Bron, S.; Broulliet, S.; Eruschi, C.V.; Caldwell, B.; Capuano, V.; Carter, N.M.; Chd
A.; Ehrlich, S.D.; Emmerson, P.T.; Entian, K.D.; Errington, J.; Febret, C.; Ferrari, E.
Nature 390, 249-256, 1997
A; Authors: Foulger, D.; Fritz, C.; Fujita, M.; Fujita, Y.; Fuma, S.; Galizzi, A.; Galler
A; Authors: Foulger, D.; Fritz, C.; Fujita, M.; Fujita, X.; Empidus, A.; Galler
iech, J.; Harwood, C.R.; Henaut, A.; Hilbert, H.; Holsappel, S.; Hullo, M.F.
Koetter, P.; Koningstein, G.; Krogh, S.; Kumano, M.; Kurita, K.; Lapidus, A.; Lardinois,
A; Authors: Laudher, J.; Lazarevic, V.; Lee, S.M.; Eevine, A.; Liu, H.; Masuda, S.; Mauueell
Y, M.; Glawara, A.; Odiwara, A.; Roche, B.; Rose, M.; Sadaie, Y.; Sato, T.; Scanlon,
Rieger, M.; Rivolta, C.; Rocha, E.; Roche, B.; Rose, M.; Sadaie, Y.; Sato, T.; Scanlon,
A; Authors: Schleich, S.; Schroeter, R.; Scoffone, F.; Sekyguchi, J.; Sekwara, A.; Josato, V.;
Winters, P.; Wipat, A.; Tamamoto, H.; Tamamoto, H.; Tamamoto, H.; Tamamoto, H.; Yamamoto, K.; Yata, K.; Yoshida, R.; Attle: The complete genome sequence of the Gram-positive bacterium Bacillus subtilis.
A; Reference number: A69580; MUID:98044033
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A;Title: Complete genome sequence of the alkaliphilic bacterium Bacillus halodurans A;Reference number: A83650; MUID:20263314
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    14;
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              conserved hypothetical protein ykoN - Bacillus subtilis
C;Species: Bacillus subtilis
C;Date: 05-Dec-1997 #sequence_revision 05-Dec-1997 #text_change 15-Oct-1999
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C.Date: 01-Dec-2000 #sequence_revision 01-Dec-2000 #text_change 31-Dec-2000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           285 KRLPVFIYHALPGQEEMNLNLLHERKL--VTDMRNWDMQKAEEYIAAFFQSNEQMKEYKK 342
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    173 KVTGIPIDNKFETPINQKQWLIDNNLDPDKQTILMSAGAFGVSKGFDTMITDILAKSANA
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23.5%; Pred. No. 4.9e-11;
Live 75; Mismatches 168;
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HVNGYLGEMSDRKIK 357
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Best Local S
Matches 88
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GB:AE000783; NID:g2688699; PIDN:AAC67113.1; PID:g268
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C;Accession: F70195
R;Fraser, C.M.; Casjens, S.; Huang, W.M.; Sutton, G.G.; Clayton, R.; Lathigra, R.; Son, D.; Peterson, J.; Kerlavage, A.R.; Quackenbush, J.; Salzberg, S.; Hanson, M.; Bowamn, C.; Garland, S.; Fujii, C.; Cotton, M.D.; Horst, K.; Roberts, K.; Hatch, Nature 390, 580-586, 1997
A;Authors: Smith, H.O.; Venter, J.C.
A;Tille: Genomic sequence of a Lyme disease spirochaete, Borrelia burgdorferi.
A;Reference number: A70100; MUID:98065943
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                                                                                                                                                                                                  Gaps
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                                                                                                                                                                                   6.6%; Score 136; DB 2; Length 36:
21.2%; Pred. No. 0.0082;
Live 68; Mismatches 155; Indels
                                                                                                                                                                                                  82; Mismatches 165; Indels
Score 230; DB 2;
Pred. No. 6.7e-10;
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THE	931450 Williame name; protein Yandoze cerevisiae) Williame name; protein Yandoze protein Xandoze cerevisiae) Williame name; protein Xandoze pr	D:g624033; PIDN:CAA56372.1; PID:g624034  Diest Local Similarity 19.8%; Pred. No. 0.066; Length 363; Best Local Similarity 19.8%; Pred. No. 0.066; Length 363; Best Local Similarity 19.8%; Pred. No. 0.066; Length 363; Best Local Similarity 19.8%; Pred. No. 0.066; Length 363; Best Local Similarity 19.8%; Pred. No. 0.066; Length 1157; Conservative 82; Mismatches 147; Indels 179; Gaps 27; Core 127.5; DB 2; Length 1157; Core 127.5; DB 2
10	NUP133 protein - yeast (Saccharomyces cerevisiae) NYALEROMACE names: protein YKR082w; protein YKR02C; Species: Saccharomyces cerevisiae) C; Species: Saccharomyces cerevisiae C; Date: 031 MAY-1994 #sequence_revision 03-May-1994 C; Accession: S38160; S42011; S51915; S39123 R; Baladron, V.; Ballesta, J.P.G.; Bou, G.; del Rey submitted to the Protein Sequence Database, March A; Reference number: S38158 A; Rolecule Yye: DNA A; Rolecule Yye: DNA A; Restimental source: strain S288C A; Experimental source: strain S288C A; Experimental source: strain S288C A; Title: The complete sequence of an 18,002 bp seq A; Reference number: S42011 A; Rolecule Type: DNA A; Rolecule Type: DNA A; Rolecule Type: DNA A; Rolecule Ype: DNA A; Rolecule Type: NA A; Rolecule Ype: DNA A; Rolecule Ype: DNA A; Rolecule Type: DNA A; Reference number: S1915; MUD:95112817 A; Accession: S1915	Residues: 1-1157 cboy> Cross-references: EMBL:X80066; NID:g624033; PIDN:CAA56372 Genetics: SGD:NUP133 Cross-references: SGD:S0001790; MIPS:XKR082w Map position: 11R Keywords: nucleus; transmembrane protein 413-429/Domain: transmembrane #status predicted <tmi> 641-657/Domain: transmembrane #status predicted <tmi> 641-</tmi></tmi></tmi></tmi></tmi></tmi></tmi></tmi></tmi></tmi></tmi></tmi></tmi></tmi></tmi></tmi></tmi></tmi></tmi></tmi></tmi></tmi></tmi></tmi></tmi></tmi></tmi></tmi></tmi></tmi></tmi></tmi></tmi></tmi>

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A.Experimental source: strain 022
            C;Species: Mycoplasma mycoides
C;Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 07-Dec-1999
C;Accession: S35481; S27591
S;Samuelsson, T.
Nucleic Acids Res. 20, 5763-5770, 1992
A;Title: A Mycoplasma protein homologous to mammalian SRP54 recognizes a hig A;Reference number: S35480; MUID:93087189
A;Accession: S35481
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-447 <SAM>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       74;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 447;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       52; Mismatches 143; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                Superfamily: signal recognition particle 54K protein
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Pred. No. 0.13;
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protein - Mycoplasma mycoides
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A; Residues: 1-359 < YAM>
                                                                                                                                                                                                                                                                                                                                                                                                 A; Genetic code: SGC3
C: Superfamily: signa
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Best Local S
Matches 79
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                    phospho-N-acetylmuramoyl-pentapeptide transferase - Aquifex aeolicus
C; Species: O'Accession: C70401
R; Deckert, G.; Warren, P.V.; Gaasterland, T.; Young, W.G.; Lenox, A.L.; Graham, D.E.; OV
N.
Nature 392, 353-358, 1998
A; Title: The complete genome of the hyperthermophilic bacterium Aquifex aeolicus.
A; Reference number: A70300; MUID:98196666
A; Accession: C70401
A; Status: preliminary: nucleic acid sequence not shown; translation not shown
A; Molecule type: DNA
A; Molecule type: DNA
A; Molecule type: DNA
A; Molecule type: Specimental source: Strain VF5
C; Genetics:
A; Gene: murg
C; Superfamily: murg protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              19;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          200 DLKSVLPKEFQVILLIGKIHYEKFKNLEGEKFR-----VMPFSLDMGLIYSASDVAISR 253
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         62 INSFKYFRNMYKGFYYSRPDKLDKCFYKYYGLNKLINLLIKEKPDLILL----TFPTPVM 117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PSTVKVTGIPIDNKFETPINQKQWLIDNNLDPDKQTILMSAGAFGVSKGFDTMITDILAK 228
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SANA-----QVVMICGK--SKELKRSLTAKFKLTRMYLILGYTKHMNEWWASSQLMITK 280
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PGGITITEGFARCIPMIFLNPAPGQELENAFY----FEEKGFGKIADTPE-----EAI 329
      214 AKP--YQFVYVTGTVHYERVQEQMKSIGQPENV----IVQPFIHNMPDVLSAVDLIVARA 267
                                                                                                                                                                                                   GGITITEGFARCIPMIFLNPAP----GQELENAFYFEEKGFGKIADTPEEAIKIVASLTN 337
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    2 VTQNKKILLITGSFGNGHMQVTQSIVNQLNDMNLDHLSVIEHDLFMEAHPILTSICKKWY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 23 VLKKEKVKFIGSKRG-----IEYELKDL-----IKTEKLFLDVEPLRE-----
                                                                                       AKSANAQVVMICG-----KSKELKRSLTAKFKLTRMYLILGYTKHMNEWMASSQLMITKP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Indels 103;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   6.0%; Score 123.5; DB 2;
20.7%; Pred: No. 0.067;
tive 72; Mismatches 131;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         118 SVLTEQFNINIPVATVMTDYRLHKNWITPYSTRYYVATKE----
                                                                                                                                                                                                                                                                                                                                                                |: | : | : : | : : GDRLLEDIDDIMVTPGRLDAMKQAAKAL 345
                                                                                                                                                                                                                                                                                                                         GNEQLIN----MISTMEQDKIKYATQTI 361
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        KEIVKNLERYSENIKKFFAEGAEERM 338
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;Gene: murG
;Superfamily: murG protein
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Matches 80; Conserv
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OY 285 TITEGFARCIPMIFLNPAPGQELENAFYFEEKGFGKIADTPEEAIKIVASLT 336 ::	Search completed: June 29, 2001, 09:00:20 Job time: 182 séc					
Db 11 VITSDSGGGAENLVSNMLDSDGLFLQ-YAIYFS 42  Qy 70 NMYKGFYYSRPDKLDKCFYKYGG	SAGAFG    : SVGSLK HMNEWM : :: ELEKFY	QY 272 ASSQLMITKPGGITITEGFARCIPMIFLNPAPGQELENAFYFEEKGF 318  1 :	RESULT 15 C64664  transferase, peptidoglycan synthesis - Helicobacter pylori (strain 26695) C; Species: Helicobacter pylori C; Species: Helicopacter pylori C; Matthey, L. Son, J.D.; Kelloy, J.M.; Cotton, M.D.; Weidman, J.M.; Fujii, C.; Bowman, C.; Watthey, L.	Alauthors: Wallin, E.; Hayes, W.S.; Borodovsky, M.; Karpk, P.D.; Smith, H.O.; Fraser, C. A; Fille: The complete genome sequence of the gastric pathogen Helicobacter pylori. A; Frile: The complete genome sequence of the gastric pathogen Helicobacter pylori. A; Reference number: A64520; MUID:97394467 A; Accession: C64664 A; Status: preliminary; nucleic acid sequence not shown; translation not shown A; Molecule type: DNA A; Residues: 1-353 < TON> A; Residues: 1-353 < TON> A; Cross-references: GB:AE000621; GB:AE000511; NID:92314301; PIDN:AAD08196.1; PID:9231436 C; Superfamily: murG protein	Query Match 5.7%; Score 117.5; DB 2; Length 353; Best Local Similarity 20.6%; Pred. No. 0.2; Matches 81; Conservative 59; Mismatches 169; Indels 85; Gaps 20; QY 11 ITGSFGNGHMQYTQSIVNQLNDMNLDHLSVIEHDLEMEAHPILTSICKKWYINSFX 67 1	Qy 68 FRNMYKGFYYSRPDKLDKCFYKYYGLNKLINLLIKEKPDLILLTFPT 114  Db 51 FSERYFFNTQGVNKSFFKKIGSLFLQAKAAFKAEILKHQITHTISVGGFSAGFA 107  QY 115 PVMSVLTEQFNININPVATVMTDYRLHKNWITPYSTRYVATKETKQDFIDVGI-DPSTVK 173    1   1   1   1   1   1   1   1   1

Mon Jul 2 09:00:17 2001

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us-09-668-788-4.rsp

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June 29, 2001, 09:04:10 ; Search time 16.33 Seconds (Without alignments) 820.202 Million cell updates/sec
GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
                                                                                          OM protein - protein search, using sw model
                                                                                                                                         Run on:
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US-09-668-788-4 2048 1 MVTQNKKILLITGSFGNGHM.....SSQPQEIYGKVPLYARFFVK 391 Title: Perfect score: Sequence:

93435 seqs, 34255486 residues Searched:

BLOSUM62 Gapop 10.0 , Gapext 0.5

Scoring table:

93435 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

SwissProt\_39:\* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

		di			SUMMARIES	
Result		Query				
Q	Score	Match	Match Length	DB	Ωī	Description
-	591.5	28.9	382	П	YPFP_BACSU	
7	136	٠	363	Н	MURG_BORBU	borrelia
m	135	9.9	363	-	MURG_ENTFA	enterococ
4	127.5		1157	Н	N133_YEAST	
ς	124	6.1	352	Н	MURG_STRPN	Q9zha9 streptococc
9	123.5		344	-	MURG_AQUAE	
7	122	9.0	447	Н	SR54_MYCMY	~
89	119	5.8	531	~	UD17_RAT	m
6	117.5	5.7	353	Н	MURG_HELPY	0
10	116.5	5.7	353	~	MURG_HELPJ	
11	113	5.5	950	7	Y511_RICPR	9
12	111.5	5.4	360	П	MURG_ENTHR	-
13	111.5	5.4	363	-	MURG_BACSU	P37585 bacillus su
14	111.5	5.4	534	Н	UD14_HUMAN	P22310 homo sapien
15	110.5	5.4	531	Н	UD15_RAT	
16	110.5	5.4	534	П	UD13_HUMAN	P35503 homo sapien
17	109.5	5.3	533	-	UD12_KAT	
18	109	5.3	354	-	MURG_BUCAI	P57311 buchnera ap
19	108.5	5.3	532	Н	UD11_MOUSE	_
20	106.5		530	-	UD18_RAT	Q64634 rattus norv
21	106.5		531	-	UD13_RAT	Q64637 rattus norv
22	106		339	-	MURG_THEMA	Q9wy74 thermotoga
23	106		530	Н	UDBF_HUMAN	P54855 homo sapien
24	106		530	-	UDBK_MACFA	
25	105.5	5.2	273	-	SP0A_CLOPA	P52940 clostridium
26	104.5	5.1	529	П	UD16_RAT	
27	104		1196	Т	BXCN_CLOBO	P46081 clostridium
78	103.5		484	Η.	YA62_METJA	Q58462 methanococc
53	102.5		532	-	UD14_RABIT	Q28612 oryctolagus
30	102.5		934	<b>-</b>	- 1	
31	102		530	-	UDBH_HUMAN	075795 homo sapien
32	102	2.0	798	<b>—</b>	- 1	P30003 human herpe
33	101.5	5.0	376	-	WECB_ECOLI	_

Q64550 rattus norv Q08582 sulfolobus	P52437 human herpe P70691 mus musculu	P10486 escherichia	Q95666 pinus strob	Q64435 mus musculu	P35504 homo sapien	P22309 homo sapien	051528 borrelia bu	P09333 bacillus br	P46741 prototheca
UD11_RAT TOPG_SULAC	V120_HSV6U UD12_MOUSE	T1R1_ECOLI	CHLB_PINST	UD16_MOUSE	UD15_HUMAN	UD11_HUMAN	RECG_BORBU	SLPO_BACBR	RT02_PROWI
	~~	Н	Н	Н	П	7	Η	П	1
535 1248	1082	1033	511	531	534	533	989	1004	274
5.0	<b>44</b> 0.0.	4.9	4.9	4.9	4.9	4.9	4.8	4.8	4.8
101.5	101	100.5	100	100	100	99.5	66	66	98.5
3.5 3.5	36	38	33	40	41	42	43	44	45

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SECUENCE FROM N.A.
SETRAINS—ATCC 35210 / B31;
MEDLINE—80605943; PubMed=9403685;
Fraser C.M., Casjens S., Huang W.M., Sutton G.G., Clayton R.A.,
Lathigra R., White O., Ketchum K.A., Dodson R., Hickey E.K., Gwinn M.,
Dougherty B., Tomb J.-F., Fleischmann R.D., Richardson D.,
Peterson J., Kerlawage A.R., Quackenbush J., Salzberg S., Hanson M.,
van Vugt R., Palmer N., Adams M.D., Gocayne J.D., Weldman J.,
Ulterbock T., Watthey L., McDonald L., Artiach P., Bowman C.,
Sanith H.O., Venter J.C.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TATURE 390:580-586(1997).

"INTERMEDIATE I) TO FORM UNDECAPRENTL-PYROPHOSPHORYL-WURNAC-PENTAPEPTIDE (LIPID INTERMEDIATE I) TO FORM UNDECAPRENTL-PYROPHOSPHORYL-MURNAC-FENTEDS-GLEUARC (LIPID INTERMEDIATE I) EY SIMILARITY).

"INTERMEDIATE IS TO FORM TO FORM
                                                                                                              285
                                                                                                                                                                      285
                                                                                                                                                                                                                                345
                                                                                                                                                                                                                                                               30-MAY-2000 (Rel. 39, Last sequence update)
30-MAY-2000 (Rel. 39, Last annotation update)
UDP-N-ACETYLGLUCOSAMINE--N-ACETYLMURANYI-(PENTAPEPTIDE)
PYROPHOSPHORYL-UNDECAPRENOL N-ACETYLGLUCOSAMINE TRANSFERASE
(EC. 2.4.1.-) (UNDECAPRENYI-PP-MURNAC-PENTAPEPTIDE-UDPGICNAC GLCNAC
                           PIDNKFET----PINQKQWLIDNNLDPDKQTILMSAGAFGVSKGFDTMITDILAKSANA
                                                                                                                 QVVMICGKSKELKRSLTA-----KFKLTRMYLILGYTKHMNEWMASSQLMITKPGGIT
                                                                                                                                                                                                                                286 ITEGFARCIPMIFLNPAPGQELENAFYFEEKGFGKIADTPEEAIKIVASLINGNEQLINM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Transferase; Glycosyltransferase; Cell division; Cell wall;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Genomic sequence of a Lyme disease spirochaete, Borrelia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Membrane: Peptidoglycan synthesis.
SEQUENCE 363 AA; 41118 MW; 1BAFA347384DB235 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Borrella burgdorferi (Lyme disease spirochete).
Bacteria: Spirochaetales; Spirochaetaceae; Borrella.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           363 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                             346 KKNIKDLHLANSSEVILEDIL 366
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(Rel. 39, Last seq
(Rel. 39, Last ann
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EMBL; AE001176; AAC67113.1; -.
                                                                                                                                                                                                                                                                                                                                                     346 ISTMEQDKIKYATQTICRDLL 366
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STANDARD;
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Gaps

96;

DB 1; Length 363;

6.6%; Score 136; DB 1; Length 36 21.2%; Pred. No. 0.0029; Live 68; Mismatches 155; Indels

Conservative

Query Match Best Local Similarity Matches 86; Conserv

Best\_Loc Matches

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                                                                                                                                                                                                                                                                                 107 FVSTPAIIASSLLKIKSITHEMDLDPGLATKIN-----SKFANNIHISFKESEKYF 157
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ------LNPDPKIIKQLTQNTNKPIISILGG 199
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30-MXY-2000 (Rel. 39, Last sequence update)
30-MXY-2000 (Rel. 39, Last annotation update)
40-MY-2000 (Rel. 39, Last annotation update)
50-MY-2000 (Rel. 39, Last annotation update)
60-MY-2000 (Rel. 39, Last annotatio
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Bacteria; Firmicutes; Bacillus/Clostridium group; Enterococcaceae;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    163 IDVGIDPSTVKVTGIPIDNKFETPINQKQWLIDNNLDPDKQTILMSA-----GAFGV
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--- LDHLSVIEHDLFMEAHPI -- LTS
                                                                        3 NKKIIFFTGGGTGGHVFPGISIIQKLKEFDNEIEFFWIGKKNSIEEKLIKEQDNIKFISI
                                                                                                                                                                                                              ICKKW--YINSFKYFRNMYKGFYYSRPDKLDKCFYKYYGLNKLINLLIKEKPDLILLT--
                                                                                                                                                                                                                                                                                                                                                                                                                       112 -FPTPV------MSVLTEQFNINIPVATVMTDYRLHKNWITPYSTRYYVATKETKQDF
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Transferase; Glycosyltransferase; Cell division; Cell wall;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     322 ADTPEEAIKIVASLINGNEQLINMISTMEQDKIKYATQTICRDLL 366
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   363
           NKKILLITGSFGNGHMQVTQSIVNQLNDMN----
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MEDLINE=97431524; PubMed=9287029;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          158 KNY ----KNIIYTGSPIRREF --
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MURG_STRPN
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SIMILAR
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MURG_STRPN
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                                                                         16;
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--- FUNCTION: INVOLVED IN POLY(A)+ RNA TRANSPORT AND NUCLEAR PORE
                                                                                                                                                                                                                                                               Doye V., Wepf R., Hurt E.C.;
"A novel nuclear pore protein Nupl33p with distinct roles in poly(A)+
RNA transport and nuclear pore distribution.";
EMBO J. 13:6062-6075(1994).
                                                                                                                                                                                             109 ILTFPTPVMSVLTEQFNINIPVATVMTDYRLHKNWITPYSTRYY------VATKETK 159
                                                                                                                                                                                                              160 QDFIDVGIDPSTVKVTGIPIDNKFETPINQKQWLIDNNLDPDKQTILM---SAGAFGVSK 216
                                                                                                                                                                                                                                                                                            217 GFDTMITDILAKSANAQVVMICGKS--KELKRSLTAKFKLTRMYLILGYTKHMNEWMASS 274
                                                                                                                                                                                                                                                                                                            275 QLMITKPGGITITEGFARCIPMIFLNPAP----GQELENAFYFEEKG-FGKIADTPEEAI 329
                                                                                                                                               -------FRNM-YKGFYYSRPDKLDKCFYKYY-GLNKLINLLIKEKPDLI 108
                                                                         Gaps
                                                                                                                                                               37 GTENGLESQIVPKAKIPFKTIKIQGFKRSLSPQNFKTIYLFLTSINKAKKIIREFQPDVV 96
                                                                                                              9 LIITGSFGNGHMQVTQSIVNQLNDMNLDHLSVIEHDLFMEAHPILTSICKKWYINSFKY- 67
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Saccharomyces cerevisiae (Baker's yeast).
Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
Saccharomycetales; Saccharomycetaceae; Saccharomyces.
                                                                        84;
                                              6.6%; Score 135; DB 1; Length 36
20.6%; Pred. No. 0.0035;
ive 75; Mismatches 161; Indels
           5178BCC95264BE69 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                            330 KIVASLTN---GNEQLTNMISTMEQDKIKYATQTICRDLLDLI 369
                                                                                                                                                                                                                                                                                                                                                                                                           01-JUN-1994 (Rel. 29, Created)
01-JUN-1994 (Rel. 29, Last sequence update)
01-CCT-1996 (Rel. 34, Last annotation update)
NUCLEOPORIN NUF133 (NUCLEAR PORE PROTEIN NUF133).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SUBCELLULAR LOCATION: NUCLEAR PORE COMPLEX.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1157
Peptidoglycan synthesis
363 AA; 39916 MW; 517
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MEDLINE-94262327; PubMed-8203164;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STRAIN-JUXJR;
MEDLINE-95112817; PubMed-7813444;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NUP133 OR YKR082W OR YKR402.
                                                         Local Similarity 20.6
les 83; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STANDARD;
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P36161;
 Membrane;
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           SEQUENCE
                                                Query Match
                                                                                                                                                                                                                                                                     155
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                27;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NLL--IKEKPDL------ILLTFPTPVMSVLTEQFNINIPVATVMTDYRL 139
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          : | | | : | | : | | | ESITDTKFKPKIFIPQMENANDTNEVTSILVMFPNAV--VITQ---VN---SKLDSSYSM 439
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   500 QAVYFSKINANPIDFNLPPEISLDQESIEHDLKLTSEEIFHSNGKYIPPMLNTLGQHLSV 559
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RKEFFQNFLTFVAKNFNYKI-----SPELKLDLIEKFEILNCCIKFNSIIRQSDVLNDI 613
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ----ILGYTKHMNEWMASSQLMITKPGGITITEGFARCIPMIFLNPAPGQELENAFYFEE 315
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        316 KGFGKLADTPEEAIKIVASLTNGNEQL--TNMISTMEQDKI-KYATQTICRDLLDLIGHS 372
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              51 PI------LTSI----CKK-WYINSFKYFRNMYKGFYYSRPDKLDKCFYKYYGLNKLI 97
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30-MAY-2000 (Rel. 39, Last sequence update)
30-MAY-2000 (Rel. 39, Last annotation update)
30-MAY-2000 (Rel. 39, Last annotation update)
90DP-N-ACETYLGLUCOSAMINE-N-ACETYLGLUCOSAMINE TRANSFERASE
PYROPHOSPHORYL-UNDECAPRENVL-PP-WURNAC-PENTAPEPTIDE-UDPGLCNAC
TRANSFERASE).
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Bacteria; Firmicutes; Bacillus/Clostridium group; Streptococcaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  -----KVTGIPIDNKFETPINQKQWLIDNNLDPDKQTILMSAGAF-----GV
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                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 1157;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Indels
                                                                                                                                                                                                                                                                                                                                   POTENTIAL.
TO NUP120 (AA 434-763).
MW; C8BDBB7D709C5C08 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             VTQNKKILIITGSFGNGHMQVTQSIVNQLNDMNLDHLSVIE---HDLF--
                                                                                                                                                                                                                                                                                                                                                                                                                                                         6.2%; Score 127.5; DB 1; 20.9%; Pred. No. 0.063; ative 67; Mismatches 147;
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                                                                                                                                                                                                                                                                                                           Nuclear protein; Transport; Transmembrane.
FRANSMEM 217 233 POTENTIAL.
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                                                                                                                                                                                                                                                                                                                                                                                     1157 AA; 133319 MW;
                                                                                                                                                   EMBL; X80066; CAA56372.1; -. EMBL; Z27116; CAA81633.1; -. EMBL; Z28307; CAA82161.1; -. PIR; S38160; S38160.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      -DPMEVDTSKLPWFINF 712
                                                                                                                                                                                                                                                                                                                                                                                                                                                         Ouery Match 6.29
Best Local Similarity 20.99
Matches 104; Conservative
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                                                                                                                                                                                                                                                                                 S0001790; NUP133.
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Query Match 6.08
Best Local Similarity 20.79
Matches 80; Conservative
                                                                                        SEQUENCE FROM N.A.
                                                                 NCBI_TaxID=63363;
                              MURG OR AQ_1177.
Aquifex aeolicus
                                                                                                                                                                      aeolicus
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                                                                                                                                                                                                                                                                                                                                                                                     19;
                                                                                                  111 TFPTPVMSVLTEQFNINIPVATVMTDYR--LHKNWITPYSTRYYVATKETKQDFIDVGID 168
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                169 PSTVKVTGIPIDNKFETPINQKQWLID--NNLDPDKQTILMSAGAFGVSKGFDTMITDIL 226
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        284 ITITEGFA----RCIPMIFLNPAPGQELENAFYFEEKGFGKIADTPEEAIKIVASLINGN 339
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     56 ICKKWYINSFKYFRNMYKGFYYSRPDKLDKCFYKYYGLNKLINLLIKEKPDLI----LL 110
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                            55
                                                                                                                                                                                                                                                                                                                                                                                                                                2 KKIVFTGGGTVGHVTLNLLLMPKFIEDGWEVHYIGDKRGIEHQEILKSGLDVTFHSIATG 61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          7 KILIITGSFGNGHMQVTQSI------VNQLND-MNLDHLSVIEHDLFMEAHPILTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            105 SVP-PVIAARVS----GVPVFIHESDLSMGLANKIAYKFATKMY-STFEQASSLSKVEHV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           227 AK-SANAQVYMICGKS--KELKRSLTAKFKLTRMYLILGYTKHMNEWMASSQLMITKPGG
                                                                                                                                                                                                                                                                                                                                                                                     74;
                                                                   Massidda O., Anderluzzi D., Friedli L., Feger G.; "Unconventional organization of the division and cell wall gene
                                                                                                                                                                                                                                                                                             EMBL; AF068902; AAC95450.1; -.
Transferase; Glycosyltransferase; Cell division; Cell wall;
                                                                                                                                                                                                                                                                                                                                                               6.1%; Score 124; DB 1; Length 352; 20.6%; Pred. No. 0.023; ve 80; Mismatches 154; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       30-MAY-2000 (Rel. 39, Created)
30-MAY-2000 (Rel. 39, Last sequence update)
30-MAY-2000 (Rel. 39, Last annotation update)
UDP-N-ACETYLGLUCOSAMINE--N-ACETYLMURAMYL-(PENTAPEPTIDE)
                                                                                                                                                                                                                                                                                                                    Membrane; Peptidoglýcan synthesis.
SEQUENCE 352 AA; 39480 MW; 75AB4EC66B2DCFAD CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    344
                                                                                          cluster of Streptococcus pneumoniae.";
Microbiology 144:3069-3078(1998).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     367
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EKLSHLLSHKEDYQAKMKASKELKSLAD 342
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EQLINMISTMEODKIKYATOTICRDLLD
                                              STRAIN=G54;
MEDLINE=99061199; Pubmed=9846742;
                                                                                                                                                                                                                                                                                                                                                                           20.6%;
                                                                                                                                                                                                                                                                                                                                                                         Local Similarity 20.6 nes 80; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STANDARD;
                                   SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MURG_AQUAE
O67238;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                62 KLRR--
                                                                                                                                                                                                                                                                                                                                                                  Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MURG_AQUAE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     340
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            315
                                                                                                                                                                                                                                                                                                                                                                                        Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RESULT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TABLE 392;353-358(1998).

-i-FUNCTION: CELL WALL FORMATION: CATALYZES THE TRANSFER OF A GLCNAC SUBUNIT ON UNDECAPRINIL-PYROPHORYL-MURNAC-PENTAPEPTIDE (LIFID INTERMEDIATE I) TO FORM UNDECAPRENYL-PYROPHOSCHORYL-MURNAC-(PENTAPEPTIDE)GLCNAC (LIPID INTERMEDIATE II) (BY SIMILARITY).

-i-SPATHWAY: LAST STEP OF PEPTIDOGLYGAN BIOSYNTHESIS.

-i-SUBGELLUTAR LOCATION: MEMBRANE ASSOCIATED (BY SIMILARITY).

-i-SIMILARITY: BELONGS TO THE MURG FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        147 PEGVRV-GLPIRKELKKKLPKKEPKRRRGLEPDKITVLI----FGGSQG--ALFLNELAR 199
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PGGITITEGFARCIPMIFLNPAPGQELENAFY----FEEKGFGKIADTPE------EAI 329
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  254 AGAGTINELSHFGVPSVFV-PYPYAVDDHQFYNAKEIEKLGGGLVLRQEEAKPDKVLSAL 312
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ------RNFYQ------KL-KAIWKFLKAQEEINEFLKEDYRALIFGGYASLPLGIN 104
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SVLTEQFNINIPVATVMTDYRLHKNWITPYSTRYYVATKE------TKQDFIDVGID 168
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          62 INSFKYFRNMYKGFYYSRPDKLDKCFYKYYGLNKLINLLIKEKPDLILL----TFPTPVM 117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         2 VIQNKKILLIITGSFGNGHMQVTQSIVNQLNDMNLDHLSVIEHDLFMEAHPILTSICKKWY 61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      <u>۲</u>
PYROPHOSPHORYL-UNDECAPRENOL N-ACETYLGLUCOSAMINE TRANSFERASE (EC 2.4.1.-) (UNDECAPRENYL-PP-MURNAC-PENTAPEPTIDE-UDPGLCNAC GLCNAC TRANSFERASE).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SANA-----QVVMICGK--SKELKRSLTAKFKLTRMYLILGYTKHMNEWMASSQLMITK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      200 DLKSVLPKEFQVILLTGKIHYEKFKNLEGEKFR-----VMPFSLDMGLIYSASDVAISF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        23 VLKKEKVKFIGSKRG------IEYELKDL-----IKTEKLFLDVEPLRE-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   105 TVLRRK------ELFIHEONSIPSKTNKILSKKAKKVLITFNYTKRFF----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PSTVKVTGIPIDNKFETPINQKQWLIDNNLDPDKQTILMSAGAFGVSKGFDTMITDILAK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Deckert G., Warren P.V., Gaasterland T., Young W.G., Lenox A.L., Graham D.E., Overbeek R., Snead M.A., Keller M., Aujay M., Huber Feldman R.A., Short J.M., Olson G.J., Swanson R.V.; The complete genome of the hyperthermophilic bacterlum Aquifex
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 344;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Transferase; Glycosyltransferase; Cell division; Cell wall;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     5A4B3322B4AC650C CRC64;
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                                                                                                                                                                                                                                             Bacteria; Aquificales; Aquificaceae; Aquifex.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               K-IVASLINGNEQLINMISTMEQDKI 354
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Membrane, Peptidoglycan synthesis.
SEQUENCE 344 AA; 39325 MW; 5A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDLINE=98196666; PubMed=9537320;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            | || :| :| : : :::
KEIVKNLERYSENIKKFFAEGAEERM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EMBL; AE000727; AAC07193.1; -.
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SKELKRSLTAKFKLTRMYL-----ILGYTKHMNEWMASSQLMITK----PGGITI 286
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EMBL; M34007; AAA42312.1; ALT_TERM.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDLINE=95332265; PubMed=7608130;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDLINE=90274676; PubMed=2112380;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (UGT1) gene complex.";
J. Biochem. 117:392-399(1995).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE OF 287-531 FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         [1]
SEQUENCE OF 1-286 FROM N.A.
                                                                                                                                                                                                                                                                                     STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Rattus norvegicus (Rat).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 InterPro; IPR002213;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          primary transcript."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           26
487
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STRAIN-WISTAR;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TRANSMEM
                                                                                                                                                                                                                                                                                                        064633
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                                                                                                                                                                                                                              80
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CHAIN
                                           203
                                                                                                  287
                                                                                                                                                                                                                                                       UD17_RAT
                                                                                                                                                                                                                                 RESULT
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                                         g
                                                                                                δ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to licenseeisb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               16;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       110
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   64 SFKYFRNMYKGFYYSRPDKLDKCFYKYYGLNKLINLLIKEKPDLILLFFPTPVMSVLFEQ 123
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   124 FNINIPVATVMTDYRLHKNWITPYSTRYYVATKETKQDFIDVGID---PSTVKVTGIPID 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           13 GSFGNGHMQ--VTQSIVNQ-LNDMNLD-----HLSVIEHDLFMEAHPILTSICKKWYIN 63
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               4 GDFLSKRMQKSIEKNMKNSTLNEENIKETLKEIRLSLLEADVNIEA-----AKEIIN 55
                                                                                                                                                                                                                                                                                                                                                                                                         SUBUNIT: SIGNAL RECOGNITION PARTICLE CONSISTS OF A 4.5 RNA MOLECOLE AND PROTEIN FFH (BY SIMILARITY).

DOMAIN: THE PROTEIN HAS A TWO DOMAIN STRUCTURE: THE G-DOMAIN BINDS GTP; THE M-DOMAIN BINDS THE RNA AND ALSO BINDS THE SIGNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SIMILARITY: BELONGS TO THE SRP FAMILY OF GTP-BINDING PROTEINS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NVK---QKALGGYISEGASAHQQMIKIVH-EELVNILGKENAPLDINKKPSVVMMVGLQ-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NKFETPINQKQWLIDNNLDPDKQTILMSAGAFGVSKGFDTMITDILAKSANAQVVMICGK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                74;
                                                                                                                                                                                                                         Bacteria; Firmicutes; Bacillus/Clostridium group; Mollicutes;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DB 1; Length 447;
                                           01-JUL-1993 (Rel. 26, Created) - 01-JUL-1993 (Rel. 26, Last sequence update) 30-MAY-2000 (Rel. 39, Last annotation update) SIGNAL RECOGNITION PARTICLE PROTEIN (FIFTY-FOUR HOMOLOG). FFH OR SRPM54.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     6.0%; Score 122; DB 1; Length 44.
22.9%; Pred. No. 0.045;
ve 52; Mismatches 143; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GTP (BY SIMILARITY).
GTP (BY SIMILARITY).
GTP (BY SIMILARITY).
24A71128D4041D43 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GTP-binding; RNA-binding.
                447 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     M-DOMAIN
                PRT;
                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
MEDLINE-93087189; PubMed=1280809;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           50100 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EMBL; M91593; AAA25441.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   particle;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              22.9%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Pfam; PF00448; SRP54; 1.
PROSITE; PS00300; SRP54; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Conservative
                STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           115
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PIR; S27591; S27591.
PIR; S35481; S35481.
HSSP; 007347; IFFH.
InterPro; IPR000897;
                                                                                                                                                                                                Mycoplasma mycoides.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               296
108
190
248
447 AA;
                                                                                                                                                                                                                                                    Entomoplasmataceae.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Signal recognition
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Similarity
                                                                                                                                                                                                                                                                                                                                                                                     Samuelsson T.B.;
                                                                                                                                                                                                                                                                             NCBI_TaxID=2102;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         80;
             SR54_MYCMY
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                HIDDAY NAME OF THE PROPERTY OF
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Pfam; PF00201; UDPGT; 1.
PROSITE; PS00375; UDPGT; 1.
Transferase; Glycosyltransferase; Glycoprotein; Transmembrane; Signal;
of a common
                                                                                                                                                                                                                                                                                                                                                     Eukāryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
NCBI_TaxID=10116;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         -i- CATALYTIC ACTIVITY: UDP-GLUCURONATE + ACCEPTOR - UDP + ACCEPTOR BETA-D-GLUCORONOSIDE.
-i- SUBCELTULAR LOCATION: MICROSOMAL.
-i- ALTERNATIVE PRODUCTS: THE UGT1 GENE ENCODES FOR MANY DIFFERENT UDPGT ISOZYMES WHICH HAVE A DIFFERENT N'TERMINAL DOMAIN AND A COMMON IC-TERMINAL DOMAIN OF 245 RESIDUES.
                                                                                                                                                                                                                  01-NOV-1997 (Rel. 35, Created)
01-NOV-1997 (Rel. 35, Last sequence update)
01-NOV-1997 (Rel. 35, Last annotation update)
01-NOV-1997 (Rel. 35, Last annotation update)
(UDP-GLUCURONOSYLTRANSFERASE 1-7 PRECURSOR, MICROSOMAL (EC 2.4.1.17)
(UDP-GLUCURONOSYLTRANSFERASE 1-7) (UGT1A7) (A2).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Biochem. Biophys. Res. Commun. 169:260-264(1990).
-!- FUNCTION: UDPGT IS OF MAJOR IMPORTANCE IN THE CONJUGATION AND SUBSEQUENT ELIMINATION OF POTENTIALLY TOXIC XENOBIOTICS AND ENDOGENOUS, COMPOUNDS.
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N-LINKED (GLCNAC. .) (POTENTIAL).

N-LINKED (GLCNAC. .) (POTENTIAL).

N-LINKED (GLCNAC. .) (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Emi Y., Ikushiro S.I., Iyanagi T.;
"Drug-responsive and tissue-specific alternative expression of
multiple first exons in rat UDP-glucuronosyltransferase family
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          -!- SIMILARITY: BELONGS TO THE UDP-GLYCOSYLTRANSFERASE FAMILY.
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                                               TEGFARCIPMIFLNPAPGQELENAFYFEE----KGFGKIADTPEEAIK 330
                                                                                 261 SISYLTKLPIKFIGEGEGYNALAAFYPKRMADRLMGMGDIETLFERAVE 309
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sato H., Kolwai O., Tanabe K., Kashiwamata S.;
"Isolation and sequencing of rat liver bilirubin UDP-
glucuronosyltransferase cDNA: possible alternate splicing
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Multigene family; Microsome; Alternative splicing.
                                                                                                                                                                                  531 AA.
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Best Local S
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STRAIN-26695 / ATCC 700392;
STRAIN-26695 / ATCC 700392;
STRAIN-27394467; PubMed-9252185;
Tomb U.-F., White O. Kerlawage A.R., Clayton R.A., Sutton G.G., Fleischmann R.D., Ketchum K.A., Klenk H.-P., Gill S., Dougherty B.A., Nelson K., Quackenbush J., Zhou L., Kirkness E.F., Peterson S., Loftus B., Richardson D., Dodson R., Khalak H.G., Glodek A., McKenney K., Fitzgerald L.M., Lee N., Adams M.D., Hickey E.K., Cotton M.D., Weidman J.M., Fujil C., Bowman C., Watthey L., Wallin E., Hayes W.S., Borodovsky M., Karp P.D., Smith H.O., Fraser C.M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                pylori.";
Nature 388:539-547(1997).
-!- FUNCTION: CELL WALL FORMATION. CATALYZES THE TRANSFER OF A GLCNAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      130 KDKKLVEYLKQSSFDAVFLDPFDVCGLTVAKYFSLPSVVFSRGIFCHYLEEGSQCPSPPS 189
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      126 INIPVATVMTDYRLHKNWITPYSTRYYVATKETKQDFIDVGIDPSTVKVTGI-----PI 179
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DNKFETPINQKQWLIDNNLDPDKQTILMSAGAFGV---SKGFDTMITDILAKSANAQVVM 236
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ICGKSKELKRSLTAKFKLTRMYLILGYTKHMNEWMASSQLM-----ITKPGGITITE 288
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GFARCIPMIFLNPAPGQELENAFYFEEKGFG -----KIADTPEEAIKIVASLTNGNEQ 341
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          379 GICHGYPMYMM-PLFGDQMDNAKRMETRGAGYTLNYLEWTADDLENALKTVINNKSYKEN 437
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ---IKEKPDLILLTFPTPVMSVLTEQFN 125
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ------LPRPVMPNVIHIGGINCHQRKPV 284
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               -----ASGEHGIVVFSLG -- SMVSEIPEKKA-MEIAE 322
                                                                                                                                                                                                                                                                                                                                                        76 TYSVSHTQEDLNR-----EFKFFIDSQWKTQQESGVLPLLTSPAQGFFELLFSHCRSLF 129
                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                              TQSIVNQLNDMNLDHLSVIEHDLFMEAH------PILTSICKKWYINSFKYFRNMY 72
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              "The complete genome sequence of the gastric pathogen Helicobacter
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Bacteria; Proteobacteria; epsilon subdivision; Helicobacter group;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        190 YVPRPILKLTDTMTFKERVWNLLSYMGEHAFCPSFFKTATDIASEVLQTPV--TMTDLFS
                                                                                                                                                                                                       160;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SUMMARY-2000 (Rel. 39, Last annotation update)
UDP-N-ACETYLGLUCOSAMINE-N-ACETYLMURAMYL-(PENTAPEPTIDE)
PYROPHORYL-UNDECAPRENOL N-ACETYLGLUCOSAMINE TRANSFERASE
(EC 2.4.1.-) (UNDECAPRENYL-PP-MURNAC-PENTAPEPTIDE-UDPGLCNAC TRANSFERASE).
                                                                                                                            Length 531;
                                                                                                                                                                                                                                                                                                                                                                                                                                           73 KG---FYYSRPDKLDKCFY------KYYGLNKLI------
        59627 MW; BC791DCE724CA621 CRC64;
                                                                                                                                                                                                       70; Mismatches 123;
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                                                                                                                        Score 119;
Pred. No. 0
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30-MAY-2000 (Rel. 39, Last sequ
30-MAY-2000 (Rel. 39, Last anno
                                                                                                                            5.8%;
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438 IMR-LSSLHKDR 448
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            AA;
                                                                                                                                                                      Similarity
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025770;
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MURG_HELPY
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                                                                                                                                                                                                                  This SWISS-PROT entry is copyright. It is produced through a collaboration
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SUBUNIT ON UNDECAPRENYL-PYROPHOSPHORYL-MURNAC-PENTAPEPTIDE (LIPID INTERMEDIATE I) TO FORM UNDECAPRENYL-PYROPHOSPHORYL-WURNAC-PENTAPEPTIDE)GLOCNAC (LIPID INTERMEDIATE II) (BY SIMILARITY). PATHWAY: LAST STEP OF PEPTIDOGIVCAN BIOSYNTHESIS. SUBCELLULAR LOCATION: MEMBRANE ASSOCIATED (BY SIMILARITY). SIMILARITY: BELONGS TO THE MURG FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              IITEGFARCIPMIFLNPAP----GQELENAFYFEEKGFGKIAD----TPEEAIKIVASLT 336
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FSERY---FFNTQGVVNKSFFKKIGSLFLQAKAAFKAKEILKKHQITHTISVGGFSAGPA 107
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ITGSFGNGHMQVTQSIVNQLNDMNLDHL---SVIEHDLFMEAHPILTSICKKWYINSFKY 67
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      UDP-N-ACETYLGUCOSAMINE--N-ACETYLMURANYL (PENNAPEPTIDE)
PYROPHOSPHORYL-UNDECAPRENOL N-ACETYLGLUCOSAMINE TRANSFERASE
(EC 2.4.1.-) (UNDECAPRENYL-PP-MURNAC-PENTAPEPTIDE-UDPGLCNAC GLCNAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Helicobacter pylori J99 (Campylobacter pylori J99).
Bacteria; Proteobacteria; epsilon subdivision; Helicobacter group;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               155 LTSYPVQNAFFDFARTRTEIKH------ILFLGGSQGAKAINEFALLNAPK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SVWELCANGLPTIFI-PYPFASNNHQYYNVLEFEKENLCYVVPQNELLPKKLFEVIRKLN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LTGGGTGGHLSIAKALAIELEKQGIEAIYLGSTYGQD-------KEWFENS-PL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FRNMYKGFYYSRPDKLDKCFYKYYG---LNKLINLLIKE--KPDLILLTF-----PT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               115 PVMSVLTEQENINIPVATVMTDYRLHKNWITPYSTRYYVATKETKQDFIDVGI-DPSTVK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SFASLLNK-----IPL----YIHEQNAIKGSLNRY--LSPKAKAVFSSYAFKDKGNHV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LAKSANAQVVMICG-KSKELKRSLTAKFKLTRMYLILGYTKHMNEWMASSQLMITKPGGI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     174 VTGIPIDNKF-----ETPINQKQWLIDNNLDPDKQTILMSAGAFGVS--KGFDTMITDI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       85;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 353;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Transferase; Glycosyltransferase; Cell division; Cell wall;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          169; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Membrane; Peptidoglýcan synthesis.
SEQUENCE 353 AA; 39474 MW; 6D136CD92A180513 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DB 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          5.7%; Scc. No. v.. 20.6%; Pred. No. v.. .. .. 59; Mismatches 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 117.5; DB Pred. No. 0.072;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                           EMBL; AE000621; AAD08196.1; -.
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(Rel. 39,
(Rel. 40,
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NCBI_TaxID=85963;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           HP1155;
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01-OCT-2000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         260 AQSKPFLQEHFESYKIDLKILDIIPTLLNKIPDIKEIFDTLNAPNKGVMISLEKALEMVA 319
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GLNKLINLLIKEK---PDLIL-LTFPTPVMSVLTEQFNIN----IPVATVMTDYRLHKNW 143
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              | : | : | : | : | | : | | | : | | | : | | | : | | | : | | | | : | | | : | | | : | | | | : | | | : | | | : | | | : | | | : | | | : | | | : | | : | | : | | : | | : | | : | | : | | : | | : | : | | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | 
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                                                                                                                                                                                                                                                                                                           Andersson S.G.E., Zomorodipour A., Andersson J.O., Sicheritz-Ponten T., Alsmark U.C.M., Podowski R.M., Naeslund A.K., Eriksson A.-S., Winkler H.H., Kurland C.G.; "The genome sequence of Rickettsia prowazekii and the origin of mitochondria.";
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Indels 134;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     5.5%; Score 113; DB 1; Length 950; 20.4%; Pred. No. 0.61; ative 69; Mismatches 156; Indels 11
                                                         Bacteria; Proteobacteria; alpha subdivision; Rickettsiales;
Rickettsiaceae; Rickettsieae; Rickettsia.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         C047F8BCF063F715 CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MYLILGYTKHMNEWMASSQLMITKPGG----
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950 AA; 108612 MW;
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                       Rickettsia prowazekii.
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                                                                                                                                  NCBI_TaxID=782;
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Best Local Simi
Matches 92;
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                                                                                                                                                                                                                              "Genomic-sequence comparison of two unrelated isolates of the human gastric pathogen Helicobacter pylori.";
Nature 397:176-180(1999).
                                                     Doig P.C.
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Alm R.A., Ling L.-S.L., Moir D.T., King B.L., Brown E.D., Doig P. Smith D.R., Noonan B., Guild B.C., deJonge B.L., Carmel G., Tummino P.J., Caruso A., Uria-Nickelsen M., Mills D.M., Ives C., Gibson R., Merberg D., Mills S.D., Jiang Q., Taylor D.E., vovis G
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                95;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DB 1; Length 353;
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Transferase; Glycosyltransferase; Cell division; Cell wall;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        63; Mismatches 162; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Membrane; Peptidoglycan synthesis.
SEQUENCE 353 AA; 39506 MW; 1773AD7E5C214EF9 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           30-MAY-2000 (Rel. 39, Created)
30-MAY-2000 (Rel. 39, Last sequence update)
30-MAY-2000 (Rel. 39, Last annotation update)
HYPOTHETICAL PROTEIN RP511.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       5.7%; Score 116.5; DB 19.8%; Pred. No. 0.086;
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nes 79; Conservative
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Q9ZD36;
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195 280 RESULT 11 Y511\_RICPR

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             17;
                                                                                                                                                                                    Duez C., Thamm I., Sapunaric F., Coyette J., Ghuysen J.-M.; "The division and cell wall gene cluster of Enterococcus hirae $185."; DNA Seq. 9:149-161(1998).
                                                                                                                                                                                                                          -1- FUNCTION: CELL WALL FORMATION. CATALYZES THE TRANSFER OF A GLCNAC SUBUNIT ON UNDECAPRENYL-PYROPHOSPHORYL-MURNAC-PENTAPEPTIDE (LIPID INTERMEDIATE 1) TO FORM UNDECAPRENYL-PYROPHOSPHORYL-MURNAC- (PENTAPEPTIDE)GLCNAC (LIPID INTERMEDIATE 11) (BY SIMILARITY).
-1- PATHWAY: LAST STEP OF PEPTIDOGLYCAN BIOSYNTHESIS.
-1- SUBCELLULAR LOCATION MEMBRANE ASSOCIATED (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              231
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30-WAY-2000 (Rel. 39, Last annotation update)
UDP-N-ACETYLGLUCOSAMINE--N-ACETYLMURAMYL-(PENTAPEPTIDE)
PYROPHOSPHORYL-UNDECAPRENOL N-ACETYLGLUCOSAMINE TRANSFERASE
(EC. 2.4.1.-) (UNDECAPRENYL-PP-WURNAC-PENTAPEPTIDE-UDPGLCNAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        57 CKKWYINSFKYFRNMYKGFYYSRPDKLDKCFYKYYGLNKLINLLIKE-KPDLILLTFPTP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             9 LIITGSFGNGHMQVTQSIVN--QLNDMNLDHLSV----IEHDLFWE-AHPILT----SI
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   292 RCIPMIFLNPAP----GQELENAFYFEEKGFGKIADTPE-----EAIKIVASLINGNE
                                                                               Enterococcus hirae.
Bacteria; Firmicutes; Bacillus/Clostridium group; Enterococcaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     104 SGAVVYAASKLAIP--TIIHEQNSVPGITNKFLSRYVDRIALSFEDAAPFF----PAEK
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              63;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 360;
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Transferase; Glycosyltransferase; Cell division; Cell wall;
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SEQUENCE 360 AA; 39591 MW; 444D6F7CFEC1FDA1 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ; Pred. No. 0.21;
81; Mismatches 170;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DB 1;
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                                                                                                                                                                          MEDLINE=99449055; PubMed=10520745;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Local Similarity 19.5
les 76; Conservative
                                                                                                                                                 SEQUENCE FROM N.A.
                                                                                                                      NCBI_TaxID=1354;
                                                                                                           Enterococcus
                                                     (RANSFERASE)
                                                                                                                                                              STRAIN-S185
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Bacteriol. 171:6821-6834(1989).

FUNCTION: CELL WALL FORMATION. CATALYZES THE TRANSFER OF A GLUNAC SUBUNIT ON UNDECAPRENYL-PYROPHOSPHORYL-WURNAC-PENTAPEPTIDE (LIFID INTERNEDIATE I) TO FORM UNDECAPRENYL-PYROPHOSPHORYL-WURNAC-(PENTAPEPTIDE)GLUNAC (LIFID INTERNEDIATE II).

(PENTAPEPTIDE)GLUNAC (LIFID INTERNEDIATE II).

- SATHWAYT: LAST STEP OF PEPTIDOGLYCAN BIOSYNTHESIS.

- SUBCELLULAR LOCATION: MEMBRANE ASSOCIATED (BY SIMILARITY).
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MURG_BACSU STANDARD; PRT; 363 AA.
P37854; P18578; 059247;
01-NOV-1990 (Rel. 16, Created)
30-MAY-2000 (Rel. 39, Last sequence update)
30-MAY-2000 (Rel. 39, Last annotation update)
90-MAY-2000 (Rel. 39, Last annotation update)
PDP-N-ACETYLGLUCOSAMINE-N-ACETYLGLUCOSAMINE-PEPTIDE)
PYROPHOSPHORYL-UNDECAPRENOL N-ACETYLGLUCOSAMINE TRANSFERASE
(EC 2 4 1.1-) (UNDECAPRENYL-PP-MURNAC-PENTAPEPTIDE-UDPGLCNAC GLCNAC TRANSFERASE)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Kobayashi Y.;
"Sequence of the Bacillus subtilis homolog of the Escherichia coli
cell-division gene murG.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       35;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Henriques A.O., de Lencastre H., Piggot P.J.; "A Bacillus subtilis morphogene cluster that includes spoVE is homologous to the mra region of Escherichia coli."; Biochimie 74:735-748(1992).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 363;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Miyao A., Yoshimura A., Sato T., Yamamoto T., Theeragool G., Robayashi Y.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Transferase; Glycosyltransferase; Cell division; Cell wall;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Beall B., Lutkenhaus J.;
"Nucleotide sequence and insertional inactivation of a subtilis gene that affects cell division, sporulation, temperature sensitivity.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              -> G (IN REF. 1).
-> T (IN REF. 1).
185B20688C732489 CRC64;
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                                                                                                                                                                                                                                                                                                                                       Bacteria; Firmicutes; Bacillus/Clostridium group; Bacillus/Staphylococcus group; Bacillus.
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Pred. No. 0.21;
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MEDLINE=92380484; PubMed=1387377;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDLINE=93003529; PubMed=1391053;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SubtiList; BG10227; murG.
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Gene 118:147-148(1992).
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Best Local Similarity
Matches 55; Conserv
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                                                                                                                                                                                                                                                                                                                       Bacillus subtilis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                            NCBI_TaxID=1423;
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Query Match
Best Local Similarity
Matches, 60; Conserv
    Aono S., Yamada Y., Keino H., Hanada N., Nakagawa T., Sasaoka Y., Yazawa T., Sato H., Koiwai O.:
"Identification of defect in the genes for bilirubin UDP-glucuronosyltransferase in a patient with Crigler-Najjar syndrome type II.";
Biochem. Biophys. Res. Commun. 197:1239-1244(1993).
                                                                                                                       MEDLINE-92147680; PubMed-1339448;
Ritter J.K., Chen F., Sheen Y.Y., Tran H.M., Kimura S., Yeatman M.T.,
GLNKLINLLIKEKPDLILLTFPTPVMSVLTEQFNINIPVATVMTDYR----LHKNWITPY 147
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               VARTANT CN-I PHE-376.
MEDLINE-9233903; Pubmed-1634050;
Bosma P.J., Chowdhury J.R., Huang T.-J., Lahiri P., Elferink R.P.J.O.
Van Es H.H.G., Lederstein M., Whitington P.F., Jansen P.L.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Chowdhury N.R.; "Mechanisms of inherited deficiencies of multiple UDP-glucuronosyltransferase isoforms in two patients with Crigler-Najjar
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            VARIANT CN-II ARG-332.
MEDLINE-94102756; Pubmed-8276413;
MGDIANE-94102756; Pubmed-8276413;
MGDIANEJI N., Clarke D.J., Boxer M., Burchell B.;
Midentification of an A-to-G missense mutation in exon 2 of the UGT1
gene complex that causes Crigler-Najjar syndrome type 2.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             01-AUG-1991 (Rel. 19, Last Sequence update)
01-GCT-2000 (Rel. 40, Last annotation update)
01-GCT-2000 (Rel. 40, Last annotation update)
(UDP-CLUCURONOSYLTRANSFERASE 1-4 PRECURSOR, MICROSOMAL (EC 2.4.1.17)
(UDPGT) (UGT-1D) (UGT1-4) (UGT1-4) (UGT1-4) (UGT1-4)
(BILIRUBIN SPECIFIC ISOZYME 2) (HUG-BR2).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       other UDP-glucuronosyltransferase isozymes with identical carboxyl
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Ritter J.K., Crawford J.M., Owens I.S.;
"Cloning of two human liver billrubin UDP-glucuronosyltransferase
CDNAs with expression in COS-1 cells.";
J. Biol. Chem. 266:1043-1047(1991).
                                                                                        148 STRYYVATKETKQDFIDVGIDPS-TVKVTGIPIDNKFETPINQKQWLIDNNLDPDKQTIL
                                                                                                                                                                                207 MSAGAFGVSKG---FDTMITDI--LAKSANAQVVMICGK-----SKELKRSLTAKFKLT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               complex locus UGT1 encodes human bilirubin, phenol,
                                                                                                                                                                                                                                                                                                     ::| | | | :: | :| | | 247 KPL----HQMPEYLKAIDVIVARAGAATIAEITALGIPSVLI-PSP 288
                                                                                                                                                                                                                                                                         256 RMYLILGYTKHMNEWMASSQLMITKPGGITITEGFARCIPMIFLNPAP 303
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A., AND TISSUE SPECIFICITY. MEDLINE-92147680; Pubmed-1339448;
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MEDLINE-94107323; PubMed-8280139;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                               01-AUG-1991 (Rel. 19, Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             syndrome, type I.";
FASEB J. 6:2859-2863(1992).
                                                                                                                                                                                                                                                                                                                                                                                                                                    STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Homo sapiens (Human)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FISSUE-Liver;
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P22310;
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation-the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                       -!-!INDUCTION: BY PHENOBARBITAL.
-!-!INDUCTION: BY PHENOBARBITAL.
-!-!DISEASE: THE GILBERT'S SYNDROME IS SHOWN TO OCCUR AS A CONSEQUENCE OF REDUCED BILLINGBIN TRANSFERASE ACTIVITY. THE DISORDER, IS MOST OFTEN DETECTED IN YOUNG ADULTS WITH VACUE NONSPECIFIC COMPLAINTS.
A MORE, SEVERE INHERITABLE DEFICIENCY IN BILLINUBIN ACTIVITY EXIST.
-IN CRICLER-NAJJAR (CN): PATIENTS WITH TYPE I (RECESSIVE TRAIT) HAVE SEVERE HYPERBILLINDINEMIA AND USDALLY DIE OF KERNICTERUS (BILLINUBIN ACCUMULATION IN THE BASAL GANGLIA AND BRAINSTEM NUCLEI) WITHIN THE FIRST YEAR OF LIFE. PATIENTS WITH TYPE II (DOMINANT TRAIT), HAVE LESS SEVERE HYPERBILLINDINEMIA AND USGALLY SURVIVE INTO ADDULTHOOD WITHOUT NEUROLGIC DAMAGE. PHENOBARBITAL, WHICH INDUCES THE PARTIALLY DEFICIENT GLUCURONYL TRANSFERASE, CAN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Pfam; PF00201; UDPGT; 1.
PROSITE; P$00375; UDPGT; 1.
PROSITE; P$00375; UDPGT; 1.
Pranaferase; Glycoprotein; Transmembrane; Signal;
                                                                                                                                                                                           -i- CATALYTIC ACTIVITY: UDP-GLUCURONATE + ACCEPTOR = UDP + ACCEPTOR = BETA-D-GLUCORONOSIDE.
-i-SUBCELLULAR LOCATION: MICROSOMAL.
-i-ALTERNATIVE PRODUCTS: THE UGT1 GENE ENCODES FOR MANY DIFFERENT UDPGT ISOZYMES WHICH HAVE A DIFFERENT N-TERMINAL DOMAIN AND A COMMON C-TERMINAL DOMAIN OF 245 RESIDUES.
-i-TISSUE. SPECIFICITY: EXPRESSED IN LIVER. NOT EXPRESSED IN SKIN OR KIDNEY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Multigene family: Microsome; Alternative splicing; Disease mutation. SIGNAL 1 28 POTENTIAL. CHAIN 29 534 UDP-GLUCURONOSYLTRANSFERASE 1-4.
Genomics 18:171-173(1993).

-!-|FUNCTION: UDPGT IS OF MAJOR IMPORTANCE IN THE CONJUGATION AND SUBSEQUENT ELIMINATION OF POTENTIALLY TOXIC XENOBIOTICS AND ENDOGENOUS COMPOUNDS. GLUCURONIDATES BILIRUBIN IX-ALPHA TO FORM BOTH THE IX-ALPHA-C8 AND IX-ALPHA-C12 MONOCONJUGATES AND DICONJUGATE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          POTENTIAL.

N-LINKED (GLCNAC. .) (POTENTIAL).

N-LINKED (GLCNAC. .) (POTENTIAL).

N-LINKED (GLCNAC. .) (POTENTIAL).

L -> P (IN CRIGLER-NAJJAR TYPE II).

/FTIG-VAR_009506.

Q -> R (IN CRIGLER-NAJJAR TYPE II).

/FTIG-VAR_007710.

S -> F (IN CRIGLER-NAJJAR TYPE II).

/FTIG-VAR_007711.
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AB745D46F57538BE CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDLINE-90274676; PubMed-2112380;
Sato H., Kolwal O., Tanabe K., Kashiwamata S.;
Sato H., Kolwal O., Tanabe K., Kashiwamata S.;
"Isolation and sequencing of rat liver bilirubin UDP-
primary transferrase CDNA: possible alternate splicing of a common primary transcript.";
Biochem. Biophys. Res. Commun. 169:260-264(1990).
-!- FUNCTION: UDPGT IS OF MAJOR IMPORTANCE IN THE CONJUGATION AND SUBSEQUENT ELIMINATION OF POTENTIALLY TOXIC XENOBIOTICS AND ENDOGENOUS COMPOUNDS.
                                 251
                                                                                                                                                     153 VATKETKQDFI---DVGIDPSTVKVTGI-----PIDNKFETPINQKQWLIDNNLDPDKQ 203
LNKLINLLIKEKPDLILLTFPTPVMSVLTEQFNINIPVATVMTDYRLHKNWITPYSTRYY 152
                                                                                                                                                                                                                                    347 ANNT-ILVKWLPQNDLLGHPMTRAFITHAGSHGVYESICNGVPMVMM-PLFGDQMDNAKR 404
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Eukaryotz, Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus. NCBL_TaxID=10116;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CATALYTIC ACTIVITY: UDP-GLUCURONATE + ACCEPTOR = UDP + ACCEPTOR
                                                                                                                                                                                                                                                                                                                                                                                                                01-NOV-1997 (Rel. 35, Created)
01-NOV-1997 (Rel. 35, Last sequence update)
01-NOV-1997 (Rel. 35, Last annotation update)
UDP-GLUCURONOSYLTRANSFERASE 1-5 PRECURSOR, MICROSOWAL (EC 2.4.1.17)
(UDP-GLUCURONOSYLTRANSFERASE 1-5 PRECURSOR, MICROSOWAL (EC 2.4.1.17)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SUBCELLULAR LOCATION: MICROSOMAL.
ALTERNATUR PRODUCTS: THE UGTI GENE ENCODES FOR MANY DIFFERENT UDPGT ISOZYMES WHICH HAVE A DIFFERENT N-TERMINAL DOMAIN AND A COMMON C-TERMINAL DOMAIN OF 245 RESIDUES.
                                                                                    204 TILMSAGAFGV---SKGFDTMITDILAKSANAQVVMICGKSKELKRSLTAKFKLTRMYLI
                                                                                                                                                                                                    LGYTKHMNEWMASSQLM-----ITKPGGITITEGFARCIPMIFLNPAPGQELENAFY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Emi Y., Ikushiro S.I., Iyanagi T.; "Drug-responsive and tissue-specific alternative expression of multiple first exons in rat UDP-glucuronosyltransferase family
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SIMILARITY: BELONGS TO THE UDP-GLYCOSYLTRANSFERASE FAMILY.
                                                                                                                                                                                                                                                                                       405 METKGAGVTLNVLEMTSEDLENALKAVINDKSYKENIMR-LSSLHKDR 451
                                                                                                                                                                                                                                                                    FEEKGFG-----KIADTPEEAIKIVASLTNGNEQLTNMISTMEQDK 353
                      531 AA
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MEDLINE-95332265; PubMed-7608130;
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EMBL; M34007; AAA42312.1; ALT_TERM.
InterPro; IPR002213; -.
Pfam; PF00201; UDGGT; 1.
PROSTIE; PS00375; UDPGT; 1.
Transferase; Glycosyltransferase; Glycoprotein; Transmembrane; Signal; Multigene family; Microsome; Alternative splicing.
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POTENTIAL.
N.LINKED (GLCNAC. .) (POTENTIAL).
W, 04148CIBA6CAAC80 CRC64;
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1 MVTQNKKILIITGSFGNGHM.....SSQPQEIYGKVPLYARFFVK 391
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GenCore version 4.5 Copyright (c) 1993 - 2000 Compugen Ltd.
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Maximum Match 100%
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                                                                        OM protein - protein search, using sw model
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Gapop 10.0 , Gapext 0.5
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SPTREMBL\_16:\*
1: Sp\_archea:\*
2: sp\_bacteria:\*
3: sp\_fungi:\*
4: sp\_human:\*
5: sp\_invertebrate:\*
5: sp\_invertebrate:\*
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6: sp\_phage:\*
7: sp\_phage:\*
7: sp\_plant:\*
7: sp\_plant:\*
7: sp\_plant:\*
7: sp\_plant:\*
7: sp\_nodent:\*
7: sp\_nodent:\* sp\_unclassified:\*
sp\_vertebrate:\*
sp\_virus:\*

Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

	Description	086492 staphylococ	Q9s193 arabidopsis	Q9fzl5 arabidopsis	Q9rvf3 deinococcus	082730 arabidopsis	Q9mu68 arabidopsis	081770 arabidopsis	P93115 cucumis sat	Q9sm44 spinacia ol	Q9fz14 qlycine max	Q9fzl3 nicotiana t	034625 bacillus su	Q9kbh0 bacillus ha	Q9ex00 streptomyce		09k9t0 bacillus ha	087161 vibrio chol	018777 oryctolagus	058652 methanococc
SUMMARIES	ΔΙ	086492	0 Q9SI93	0 Q9FZL5	Q9RVF3	0 082730	Q9MU68	0 081770	0 P93115	0 Q9SM44	0 Q9FZL4	0 Q9FZL3	034625	о9квно	Q9EX00	098519	Q9K9T0	087161	018777	058652
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	Score	2048	309	309	299	296.5	284	284	283	279.5	279.5	278	245	230	194.5	139	124	121	116	115.5
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Q01072 O51410 Q9FB02 O06038 Q9YCSO O16917 Q23334	Q9WT34 Q9L4H3 P97886 Q45916 Q53550		Q9FDJ3 O67183 O Q9XG35 O18736 Q9TSM0
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## ALIGNMENTS

RESULT 086492	1.1 1.3.2.1 1.2.1
AC AC	086492 PRELIMINARY; PRT; 391 AA. 086492;
TO	01-NOV-1998 (TrEMBLrel. 08, Created) 01-NOV-1998 (TrEMBLrel. 08, Last sequence update) 01-NAR-2001 (TrEMBLrel. 16, Last annotation undate)
DE	
SO	Staphylococcus aureus.
38	<pre>Bacteria; Firmicutes; Bacillus/Clostridium group; Bacillus/Staphylococcus group; Staphylococcus.</pre>
R OX	NCBI_TaxID*1280; [1]
RP	SEQUENCE FROM N.A.
X X	SIRAIN=COL; MEDI.INE=98313013: PubMed=9650993:
RA.	Ludovice A.M., Wu S., de Lencastre H.;
RŢ	"Molecular cloning and DNA sequencing of the Staphylococcus aureus
RT	UDP-N-acetylmuramyl tripeptide synthetase (murE) gene, essential for
RL RL	Microb. Drug Res. 4:85-90(1998).
DR	41.1;
SO	SEQUENCE 391 AA; 44703 MW; 40CDDC37A2627C6C CRC64;
č	
Ď	100.08;
Wa.	best Local Similarity 100.0%; Pred. No. 1.6e-111; Matches 391; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qγ	1 MVTQNKKILLITGSFGNGHMQVTQSIVNQLNDMNLDHLSVIEHDLFMEAHPILTSICKKW 60
Op	1 MVTQNKKILIITGSFGNGHMQVTQSIVNQLNDMNLDHLSVIEHDLFMEAHPILTSICKKW 60
Qy	61 YINSFKYFRNMYKGFYYSRPDKLDKCFYKYGLNKLINLLIKEKPDLILLTFPTPVMSVL 120
Ωp	61 YINSFKYFRNMYKGFYXSRPDKLDKCFYKYYGLNKLINLLIKEKPOLILLTFPTPVMSVL 120
Οÿ	121 TEQENINIPVATVMTDYRLHKNWITPYSTRYYVATKETKQDFIDVGIDPSTVKVTGIPID 180
QQ	121 TEQFNINIPVATVMTDYRLHKNWITPYSTRYYVATKETKQDFIDVGIDPSTVKVTGIPID 180

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281 PGGITITEGFARCIPMIFLNPAPGQELENAFYFEEKGFGKIADTPEEAIKIVAS-LINGN
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WEDLINEA20003487; PubMed=106171976

Lin X., Kaull S., Rounsley S.D., Shea T.P., Benito M.-I., Town C.D.,

Fujii C.Y., Mason T.M., Bowman C.L., Barnstead M.E., Feldblyum T.V.,

Buell C.R., Ketchum K.A., Lee J.J., Ronning C.M., Koo H., Moffat K.S.,

Croin L.A., Shen M., VanAen S.E., Unayam L., Tallon L.J., Gill J.E.,

Adams M.D., Carrera A.J., Creasy T.H., Goodman H.M., Somerville C.R.,

Copenhaver G.P., Preuss D., Nierman W.C., White O., Eisen J.A.,

Salzberg S.L., Fraser C.M., Venter J.C.;

"Sequence and analysis of chromosome II of Arabidopsis thaliana.";

Mature 402:761-768(1999).

EMBL: AC001187, AAD28678.1;

LiterPro; IPR001296;
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                                                            72 KTVLILMSDTGGGHRASAEAIRDAFKIEFGDDYRIIIKDVWKE-----YTGWPLNDM 123
                                               300
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                                                                                                                                                                                                                                                                                                                                     Eukaryota; Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta;
Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids II;
Brassicales; Brassicaceae; Arabidopsis.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    L--AKSAN--AQVVMICGKSKELKRSLTA-KFKLTRMYLILGYTKHMNEWMASSQLMITK
           SKELKRSLTAKFKLTRMYLILGYTKHMNEWMASSQLMITKPGGITITEGFARCIPMIFLN
                                                                                                              124 ERQYKFMVKHVGLWSVAFHGTSPKWIHKSYLSALAAYYA-KEIEAGLMEYKPDIIISVHP
                                                                                                 PAPGQELENAFYFEEKGFGKIADTPEEAIKIVASLTNGNEQLTNMISTMEQDKIKYATQT
NKFETPINQKQWLIDNNLDPDKQTILMSAGAFGVSKGFDTMITDILAKSANAQVVMICGK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          44;
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ICE 464 AA; 52859 MW; FEC2B424CFBBA136 CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 15.1%; Score 309; DB 10; 25.4%; Pred. No. 5e-16; iive 83; Mismatches 178;
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01-MAY-2000
01-OCT-2000
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281 PGGITITEGFARCIPMIFLNPAPGQELENAFYFEEKGFGKIADTPEEAIKIVAS-LINGN 339
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KIVLILMSDTGGGHRASAEAIRDAFKIEFGDDYRIIIKDVWKE-----YTGWPLNDM 124
                                                                                                                                                                                                                                                                                                                                                                                                                                  Arabidopsis thaliana (Mouse-ear cress).
Eukaryota, Viridiplantae, Embryophyta; Tracheophyta; Spermatophyta;
Magnollophyta; eudicotyledons; core eudicots; Rosidae; eurosids II;
Brassicales; Brassicaceae; Arabidopsis.
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LYNSKESNPIGQLIVICGRNKVLASTLASHEWKIP--VKVRGFETQMEKWMGACDCIITK
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SEQUENCE FROM N.A.
SEQUENCE FROM N.A.
Awai K., Marechal E., Block M.A., Takamiya K., Joyard J.,
"The Multigenic Family of MGDG synthases.";
"The Multigenic Family of MGDG synthases.";
SUBMITTEG (AUG-2000) to the EMBL/GenBank/DDBJ databases.
EMBL; AB047398; BAB12041.1;
SEQUENCE 465 AA; 52990 WW; 05E0157012E50A14 CRC64;
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                                                                   EQLTNMISTMEQDKIKYATQTICRDLLDLIGHSSQPQEIYGKVPLYARF
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Last annotation update)
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(TrEMBLrel, 16, I
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16,
16,
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335 LTNGNEQLTNMISTMEQDKIKYATQTICRDLLDL 368
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                                                                                                       Glycosyltransferase
58 AA; 52726 MW; 5
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                                                                                                                          468 AA;
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Best Local Similarity
Matches 103; Conserv
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Matches 100;
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Awai K., Shimojima M., Masuda T., Takamiya K.I., Ohta H.;
"CDNA cloning of an Arabidopsis monogalactosyldiacylglycerol synthase revealed that the enzyme belongs to an uridine diphosphate-utilizing
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             88 YAPWLYRGFYWLTDQDQPWNIISRMFTWLGMGAFKDELRELRPEVVINSFWAPAAVCDTL 147
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TEQFNINIPVATVMTDYRLHKNWITPYSTRYYVATKETKQDFIDVGIDPSTVKVTGIPID 180
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         232 -AQVVMIC---GKSKELKRSLTAKFKLTRMYLILGYTKHMNEWMASSQLMITKPGGITIT 287
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Eukaryota: Viridiplantae: Embryophyta; Tracheophyta; Spermatophyta;
Bagnoliophyta: eudicotyledons; core eudicots; Rosidae; eurosids II;
Brassicales; Brassicaceae; Arabidopsis.
                                                                                                                                   MEDLIRE=20036896; PubMed=10567266;
White O., Elsen J.A., Heidelberg J.F., Hickey E.K., Peterson J.D., Dodson R.J., Haft D.H., Gwinn M.L., Nelson W.C., Richardson D.L., Moffat K.S., Qin H., Jiang L., Pamphile W., Crosby M., Shen M., Vamathevan J.J., Lam P., McDonald L., Utterback T., Zalewski C., Makarova K.S., Aravind L., Daly M.J., Minton K.W., Fleischmann R.D. Ketchum K.A., Nelson K.E., Salzberg S., Smith H.O., Venter J.C.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           : | : | | | | | | | : : : | | | | | | : : | RALFMSVSLGAGHDQAQQAVKQAFAERGVELLGA-BHDSVEYLSTFERSFTVDLYEFELR
                                         Bacteria; Thermus/Deinococcus group; Deinococcales; Deinococcus.NCBI_TaxID=1299;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    32;
                                                                                                                                                                                                                                                                                     "Genome sequence of the radioresistant bacterium Deinococcus
                                                                                                                                                                                                                                                                                                                                                                                                                              Length 411;
                                                                                                                                                                                                                                                                                                                                                                                                                              14.6%; Score 299; DB 2; Length 41 25.3%; Pred. No. 2.5e-15; ive 63; Mismatches 153; Indels
                                                                                                                                                                                                                                                                                                                                                                          411 AA; 45017 MW; D825DE52B8801437 CRC64;
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01-MAR-2001 (TrEMBLrel. 16, Last annotation update)
MONOGALACTOSYLDIACYLGLYCEROL SYNTHASE (EC 2.4.1.46)
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WALL SYNTHESIS PROTEIN, PUTATIVE
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EMBL; AE001958; AAF10649.1;
TIGR; DR1076; -.
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84; Conservative
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                                 inococcus radiodurans
                                                                                                   SEQUENCE FROM N.A.
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                                                                                                                      STRAIN=R1
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                                                                                                                                                                                                                                                               112 FP----TPVMSVLTEQFNINIPVATVMTDYR-LHKNWITPYSTRYYVATKETKQDFIDVG 166
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                                                                                                                                                                                                                                                                                                                                                                                                                DMERSYKFMYKHVOLWKVAFHSTSPKWIHSCYLAAIAAYYA-KEVEAGLMEYKPEIIISV 177
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
SEQUENCE FROM N.A.
STRAIN=CV. COLUMBIA;
Jarvis P., Doermann P., Peto C.A., Lutes J., Benning C., Chory J.;
Jarvis P., Doermann P., Peto C.A., Lutes J., Benning C., Chory J.;
Jarvis P., Doermann P., Peto C.A., Lutes J., Benning C., Chory J.;
Radactoliphological Deficiency and Abnormal Chloroplast Development in the Arabidopsis MGD Synthase I Mutant.";
Proc. Natl. Acad. Sci. U.S.A. 0:0-0(2000).
                                                                                                                                                                    Gaps
                                                                                                                                                                                                                       QNKKILIITGSFGNGHMQVTQSIVNQLNDMNLDHLSVIEHDLFMEAHPILTSICKKWYIN 63
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
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Eukaryota; Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta;
Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids II;
Brassicales; Brassicaceae; Arabidopsis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           178 HPLMQEIPLWVLKWQELQKRVLFVTVITDLNTCHPTWFHPGVNRCYCPSQEVAKRALFDG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             338 LDESQVRVFGLPVRPSFARAVLVKDDLRKELEMDQDLRAVLLMGGGEGMGPVKETAKALE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        220 TMITDILAKSANAQVVMICGKSKELKRSLTA-KFKLTRMYLILGYTKHMNEWMASSQLMI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TKPGGITITEGFARCIPMIFLNPAPGQELENAFYFEEKGFGKIADTPEBAIKIV----AS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 298 EFLYDKENRKPIGOMVVICGRNKKLASALEAIDWKIP--VKVRGFETQMEKWMGACDCII
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    50;
                                                                                                 DB 10; Length 468;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 533;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        IDPSTVKVTGIPIDNKFETPINQKQWL-IDNNLDPDKQTILMSAGAFGV---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Indels
58F56C3C1C383C24 CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     01-OCT-2000 (TrEMBLrel. 15, Created)
01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
01-OCT-2000 (TrEMBLrel. 15, Last annotation update)
MONOGALACTOSYLDIACYLGLYCEROL SYNTHASE.
                                                                                          14.5%; Score 296.5; DB 10; 25.4%; Pred. No. 4.7e-15; tive 78; Mismatches 173;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    185;
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ilarity 25.5%; Pred. No. 5.4e-14;
Conservative 66; Mismatches 185;
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                               142 KKVLILMSDTGGGHRASAEAIRAAFNQEFGDEYQVFITDLWTDHTP-------WPFNQL 193
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Arabidopsis thaliana (Mouse-ear cress).
Eukaryota; Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta;
Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids II;
Brassicales; Brassicaceae; Arabidopsis.
                                                                                                                                                                                314 SQIKVYGLPVRPSFVKPVRPKVELRRELGMDENL----PAVLLMGGGEGMGPIEATARAL
                                                                                                                                                                                                                        370 ADALYDKNLGEAVGQVLIICGRNKKLQSKLSSLDWKIP--VQVKGFITKMEECMGACDCI
                                                                                                                                                                                                                                                                         KKILIITGSFGNGHMQVTQSIVNQLNDMNLDHLSVIEHDLFMEAHPILTSICKKWYINSF
                                                                               PRSYNFLVKHGTLWKMTYYGTSPRIVHQSNFAATSTFIAREIAQGLMKYQPDIIISVHPL
                                                                                                         114 ---TPVMSVLTEQFNINIPVATVMTD¥-ÅLHKNWITPYSTRYYVATKETKQDFIDVGIDP
                                                                                                                                254 MQHVPLRVLRSKGLLKKIVFTTVITDLSTCHPTWFHKLVTRCYCPSTEVAKRAQKAGLET
                                                                                                                                                                                                         219 DIMITDILAKSANAQVVMICGKSKELKRSLTA-KFKLTRNYLILGYTKHMNEWNASSQLM
                                                                                                                                                                                                                                                          278 ITKPGGITITEGFARCIPMIFLNPAPGQELENAFYFEEKGFGKIADTPEEAIKIVASLTN
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                                                         KYFRN-----MYKGFYYSRPDKL----DKCFYKYYGLNKLINLLIKEKPDLILLTFP-
                                                                                                                                                       170 STVKVTGIPIDNKFETPINQKQWL----IDNNLDPDKQTILMSAGAFGV----SKGF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.

Terryn N., Ardiles W., Buysshaert C., Dasseville R., De Clerck R.
De Keyser A., Neyt P., Rouze P., Van Den Daele H., Villaroel R.,
Gielen J., Yam Montegu M., Mewes H.W., LemcKe K., Mayer K.F.X.;
Submitted (MAR-2000) to the EMBL/GenBank/DDBJ databases.
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Submitted (MAR-2000) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              M., Hoheisel
M.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EU Arabidopsis sequencing project; submitted (MAR-2000) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                          GNEQLTNMISTMEQDKIKYATQ----TICRDLLDLI-GHSSQPQ 376
                                                                                                                                                                                                                                                                                                                       488 ---PASKELEIMSQNALRLAKPEAVFKIVHDMHELVRKKNSLPQ 528
                                                                                                                                                                                                                                                                                                                                                                                                                                01-NOV-1998 (TrEMBLrel. 08, Last sequence update)
01-MAR-2001 (TrEMBLrel. 16, Last annotation update)
MONOGALACTOSYLDIACYLGLYCEROL SYNTHASE - LIKE PROTEIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Rieger M., Mueller-Auer S., Zipp M., Schaefer
Mewes H.W., Mayer K.F.Y., Schueller C., Bevan
Submitted (JUN-1998) to the EMBL/GenBank/DDBJ
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F28M20.30 OR AT4G31780 OR MGDA.
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SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             218
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       314 SQIKVYGLPVRPSFVKPVKPKVELRRELGMDENL----PAVLLMGGGEGMGPIEATARAL 369
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               278 ITKPGGITITEGFARCIPMIFLNPAPGQELENAFYFEEKGFGKIADTPEEAIKIVASLTN 337
                                                                                                                                                                               Gaps
                                                                                                                                                                                                                    6 KKILLIITGSFGNGHMQVTQSIVNQLNDMNLDHLSVIEHDLFMEAHPILTSICKKWYINSF 65
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                                                                                                                                                                                                                                                                   KKVLILMSDTGGGHRASAEAIRAAFNQEFGDEYQVFITDLWTDHTP-------WPFNQL
                                                                                                                                                                                                                                                                                                                  KYFRN-----MYKGFYYSRPDKL----DKCFYKYYGLNKLINLLIKEKPDLILLTFP-
                                                                                                                                                                                                                                                                                                                                                  | ::| || :: | :| || 194 PRSYNFLVKHGTLWKMTYYGTSPRIVHQSNFAATSTFIAREIAQGLMKYQPDIIISVHPL
                                                                                                                                                                                                                                                                                                                                                                                                                ---TPVMSVLTEQFNINIPVATVMTDY-RLHKNWITPYSTRYYVATKETKQDFIDVGIDP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               370 ADALYDKNLGEAVGQVLIICGRNKKLQSKLSSLDWKIP--VQVKGFITKMEECMGACDCI
                                                                                                                                                                                                                                                                                                                                                                                                                                                          254 MQHVPLRVLRSKGLLKKIVFTTVITDLSTCHPTWFHKLVTRCYCPSTEVAKRAQKAGLET
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    219 DTMITDILAKSANAQVVMICGKSKELKRSLTA-KFKLTRMYLILGYTKHMNEWMASSQLM
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Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids
Cucurbitales; Cucurbitaceae; Cucumis.
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Mendel; 12656; Cucsa;1856;12656.
Transferase; Glycosyltransferase; Transit peptide; Chloroplast.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               2.4.1.46)
                                                                                                                             Length 533;
                                                                                                                                                                          Indels
                                            E581E67317CB9CC8 CRC64;
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01-JUN-1998 (TrEMBLrel. 06, Last sequence update)
01-MAR-2001 (TrEMBLrel. 16, Last annotation update)
MONOGALACTOSYLDIACYLGLYCEROL SYNTHASE PRECURSOR (EC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (1,2-DIACYLGLYCEROL 3-BETA-GALACTOSYLTRANSFERASE).
Cucumis sativus (Cucumber).
                                                                                                                                                                       66; Mismatches 185;
                                                                                                                           Score 284; DB 10;
Pred. No. 5.4e-14;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRT;
EMBL; AB047399; BAB12042.1; -.
Mendel; 32401; Arath;1856;32401
SEQUENCE 533 AA; 58537 MW; 1
                                                                                                                         13.9%;
25.5%;
                                                                                                                                                                          Conservative
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                                                                                                                                               Local Similarity
es 103; Conserv
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                                                                                                                           Query Match
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P93115;
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Matches
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183# PRSYNFLVKHGPLWKKMMYYGTSPRVIHQSNFAATSVFIAREVARGLMKYQPDIIISVHPL 242
                                                                                                                                                ---TPVMSVLTEQFNINIPVATVMTDY-RLHKNWITPYSTRYYVATKETKQDFIDVGIDP 169
                                                                                                                                                                                         243. MOHVPLRILRGRGLLEKIVFTTVVTDLSTCHPTWFHKLVTRCYCPSNEVAKRATKAGLQP 302
                                                                                                                                                                                                                                                         303 SQIKVYGLPVRPSFVRSVRPKNELRKELGMDEHLPAVLLMGGGEGMGPIEATARALGNAL 362
                                                                                                                                                                                                                                                                                                                                         GGITITEGFARCIPMIFLNPAPGQELENAFYFEEKGFGKIADTPEEAIKIVASLTNGNEQ 341
                                                                                                                                                                                                                                                                                                                                                                                                                                       421 GPGTIAEAMIRGLPIILNDYIAGQEAGNVPYVIENGIGKYLKSPKEIAKTVSQWFGPK-- 478
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    --SFK"FRN---MYKGFYY-SRPDKLDKCFYKYYG---LNKLINLLIKEKPDLILLTFP- 113
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ---TPVMSVLTEOFNINIPVATVMTDY-RLHKNWITPYSTRYYVATKETKQDFIDVGIDP 169
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          KKILLITGSFGNGHMQVTQSIVNQLNDMNLDHLSVIEHDLFMEAHPILTSICKKWYIN-- 63
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Glyc'ine max (Soybean).
Eukaryota; Viridipiantae; Embryophyta; Tracheophyta; Spermatophyta;
Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids I;
Fabales; Fabaceae; Papilionoideae; Glycine.
NCBI_TaxID#3847;
                                                                                                                                                                                                                                                                                                                 223 TDILLAKSANAQVVMICGKSKELKRSLTA-KFKLTRMYLILGYTKHMNEWMASSQLMITKP
                                                                                                                                                                                                                                   STVKVTGIPIDNKFETPINQKQWL-IDNNLDPDKQTILMSAGAFGV-----SKGFDTMI
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                                                                 KYFRN-----MYKGFYYSRPDKL----DKCFYKYYGLNKLINLLIKEKPDLILLTFP-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match 13.6%; Score 279.5; DB 10; Length 530; Best Local Similarity 25.0%; Pred. No. 1.2e-13; Matches 99; Conservative 69; Mismatches 187; Indels 41;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Awai K., Takamiya K., Ohta H.; "CDNA cloning of MGDG synthase from tobacco and soybean. Submitted (AUG-2000) to the EMBL/GenBank/DDBJ databases. EMBL; AB047475; BABL1979.1; - SEQUENCE 530 AA; 57839 WW; D33C37FD53E90218 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Created)
Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           - ANELCIMSONALKHARPDAVFKIVHDLDELV 509
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   342 LTNMISTMEQDKIKYATQ----TICRDLLDLI 369
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    01-MAR-2001 (TrEMBLrel. 16, 01-MAR-2001 (TrEMBLrel. 16, 01-MAR-2001 (TrEMBLrel. 16, MGDG SYNTHASE TYPE A.
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01-MAR-2001
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                                                                                                                                                                                                                                                                                                                                                         ---TPVMSVLTEQFNINIPVATVMTDY-RLHKNWITPYSTRYYVATKETKQDFIDVGIDP 169
                                                                                                                                                                                                                                                                                                                                                                                                                                       STVKVTGIPIDNKFETPIN-----SKQWLIDNNLDPDKQTILMSAGAFGV-----SKGF 218
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DIMITDILAKSANAQVVMICGKSKELK - - - RSLTAKFKLTRMYLILGYTKHMNEWMASSQ 275
                                                                                                                                             Gaps
                                                                                                                                                                                                               MOHVPIRILRSKGLLNKIVFTTVVTDLSTCHPTWFHKLVTRCYCPSTEVAKRALTAGLQP 307
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDLINE=99449603; PubMed=10518794)
MEDLINE=99449603; PubMed=10518794)
Miege C., Marechal E., Shinojima M., Awai K., Block M.A., Ohta H.,
Takamiya K.I., Douce R., Joyard J.,
"Blochemical and topological properties of type A MGDG synthase, a
spinach chloroplast envelope enzyme catalyzing the synthesis of both
prokaryotic and eukaryotic MGDG.";
Eur. J. Blochem. 265:990101(1999).
EMBL: AJZ49607; CAB56218.1;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Spinacia oleracea (Spinach).
Bukaryota: Viridiplantae: Embryophyta: Tracheophyta; Spermatophyta;
Magnollophyta; eudlcotyledons; core eudicots; Caryophyllidae;
Caryophyllales; Chenopodiaceae; Spinacia.
                     MONOGALACTOSYLDIACYLGLYCEROL SYNTHASE. 74FE586082EC48BA CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  KKILIITGSFGNGHMQVTQSIVNQLNDMNLDHLSVIEHDLFMEAHPILTSICKKWYINSF
                                                                                                                                                                                                                                                                      KYFRN------MYKGFYYSRPDKL----DKCFYKYYGLNKLINLLIKEKPDLILLTFP-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LMITKPGGITITEGFARCIPMIFLNPAPGQELENAFYFEEKGFGKIADTPEEAIKIVASL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     6 KKILLITGSFGNGHMQVTQSIVNQLNDMNLDHLSVIEHDLFMEAHPILTSICKKWYINSF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          336 TNGNEQLTNMISTMEQDKIKYATQ----TICRDLLDLIGHSSQPQEIYGKVPLYA 386
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FGPK---ADELLIMSQNALRLARPDAVFKIVHDLHELVKQRS-----FVPQYS 524
                                                                                                                                             60;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              41;
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                                                                                                    ; Score 283; DB 10; Length 525;
; Pred. No. 6.3e-14;
65; Mismatches 185; Indels 66
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Indels
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02E2B929732551A7 CRC64;
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Last annotation update)
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TRANSIT 1 98
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Mismatches 191;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        522 AA
CHLOROPLAST
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01-WAY-2000 (TrEMBLrel. 13, Last seq
01-WAR-2001 (TrEMBLrel. 16, Last ann
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57511 MW;
                                         57862 MW;
                                                                                                  Query Match 13.89
Best Local Similarity 25.33
Matches 105; Conservative
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  1 1
104 5
525 AA;
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**09SM44** 

RESULT Q9SM44

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Gaps

Local

Best Loc Matches

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group;

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Q9FZL3

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RA Kunst F. Ogasawara N., Moszer I., Albertini A.M., Alloni G.,
RA Acevedo V., Bertero M.G., Bessieres P., Bolotin A., Borchert S.,
RA Borriss R., Bruschi C. V., Caldwell B., Capuano V., Carter N.M.,
RA Brouillet S., Bruschi C. V., Caldwell B., Capuano V., Carter N.M.,
RA Choi S.K., Codani J.J., Connerton I.F., Cummings N.J., Daniel R.A.,
RA Choi S.K., Codani J.J., Connerton I.F., Cummings N.J., Daniel R.A.,
RA Entian K.D., Errington J.; Fabret C., Ferrari E., Foulger D.,
RA Fitz C., Fujita M., Fujita Y., Fuma S., Galizzi A., Galleron N.,
RA Ginseppi G., Guy B.J., Haga K., Halech J., Harwood C.R., Henaut A.,
RA Hilbert H., Holsappel S., Hosono S., Hullo M.F., Itaya M., Jones L.,
RA Hilbert H., Holsappel S., Hosono S., Hullo M.F., Itaya M., Jones L.,
RA Kuzita K., Lapidus A., Lardinois S., Lauber J., Lazarevic V.,
RA Kuzita K., Levine A., Liu H., Masuda G., Medina C.,
RA Medina N., Mellado R.P., Mizuno M., Mosetl D., Nakai S., Noback M.,
RA Persecan E., Pujic P., Purnelle B., Rapoport G., Rey M., Reynolds S.,
RA Fakeuchi M., Tackona E., Schoeter R., Scoffone F.,
Scanlan E., Schleich S., Schroeter R., Scoffone F.,
RA Gator M., Tacconi E., Takaqi T., Tarkmaru K.,
RA Takeuchi M., Tamakoshi A., Tanaka T., Terpstra P., Shin B.S.,
RA Tosato V., Uchiyama S., Vandelor E., Wedler F., Vasamoto R., Vatari A., Wannulet R., Wannulet R., Vasamoto R., Vatari A., Wannulet R., Wannulet R., Vasamoto R., Vatari A., Wannulet R., Wannulet R., Yasamoto R., Yannulet B., Danchin A.;
RT The complete genome sequence of the gram-positive bacterium Bacillus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PIPVMSVLTEQFNINIPVATVMTDYRLHKNWITPYSTRYYVATKETKQDFIDVGIDPSTV 172
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               6 KKILLIITG-SFGNGHMQVTQSIVNQLNDMNLDHLSVIEHDLFMEAHPILTSICKKWYINS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        65 FKYFRNMYKGFYYSRPDKL------DKCFYKYYGL--NKLINLLIKEKPDLILLT--F
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                                                                                                                                                                                                                                                         Submitted (NOV-1997) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Kunst F., Ogasawara N., Yoshikawa H., Danchin A.;
Submitted (NOV-1997) to the EMBL/GenBank/DDBJ databases.
EMBL; AJ002571; CAA05612.1; -.
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           01-MAR-2001 (TrEMBLrel. 16, Last annotation update)
                                                                                                  Bacteria; Firmicutes; Bacillus/Clostridium Bacillus/Staphylococcus group; Bacillus.
                                                                                                                                                                                                                                                                                                                                         MEDLINE=98044033; PubMed=9384377;
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EMBL; Z99110; CAB13192.1;
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Best Local Similarity
Matches 88; Conserve
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SEQUENCE FROM N.A.
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                                                                             Bacillus subtilis
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                                                                                                                                               NCBI_TaxID=1423;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               13;
                                                                                                                                                                                                                                                                                                                                                                                                                                         Nicotiana tabacum (Common tobacco).
Bukaryototi Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta;
Magnoliophyta; eudicotyledons; core eudicots; Asteridae; euasterids I;
Solanales; Solanaceae; Nicotiana.
                                                                      371 YDENIGAPVGQILVICGRNKKLANKLSSINWKVP--VQVKGFVTKMEECMGACDCIITKA 428
                                           282 GGITITEGFARCIPMIFLNPAPGQELENAFYFEEKGFGKIADTPEEAIKIVASLTNGNEQ 341
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             257 MOHVPLRILRSKGLLKKIIFTTVITDLSTCHPTWFHKLVTRCYCPSEEVAKRALRAGLKP 316
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197 PRSYNFLVKHGSLWRMTYATAPRLVHQTNFAATSTFIAREVAKGLMKYQPDIIISVHPL 256
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      114 ---TPVMSVLTEQFNINIPVATVMTDY-RLHKNWITPYSTRYYVATKETKQDFIDVGIDP 169
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STVKVTGIPIDNKFETPINQKQWL-IDNNLDPDKQTILMSAGAFGV-----SKGFDTMI 222
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        377 YDEIHGEPIGOVLVICGRNKKLFNRLTSVQWKIP--VQVKGFVTKMEECMGACDCIITKA 434
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               42;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 535;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.

Awai K., Takamiya K., Ohta H.;

"cDNA cloning of MGG synthase from tobacco and soybean.";

Submitted (AUG-2000) to the EMBL/GenBank/DDBJ databases.

EMBL, AB047476; BAB11980.1;

SEQUENCE 535 AA; 59589 WW; B1B2067E86EDE477 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Indels
                                                                                                                                                                                                                                                                                                                                                      Last sequence update)
Last annotation update)
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24.5%; Pred. No. 1.6e-13;
ive 78; Mismatches 182;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           342 LINMISTMEQDKIKYATQ----TICRDLLDLIGHSS-QPQ 376
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Created)
Last sequence update)
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                                                                                                                                                               -AYELQQMSQNALRLARPDAVFKIVHDLHELVRQRS 521
                                                                                                                                  342 LINMISTMEQDKIKYATQ----TICRDLLDLIGHSS 373
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01-MAR-2001 (TrEMBLrel 16,
01-MAR-2001 (TrEMBLrel 16,
01-MAR-2001 (TrEMBLrel 16,
MGDG SYNTHASE TYPE A.
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                                                                                                                                                                                                                                                                                    PRELIMINARY;
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NCBI_TaxID=4097;
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01-JAN-1998 (
01-JAN-1998 (
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Best Loca Matches

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Length 373;

034625

SAFE

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RESULT 034625

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Query Match
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                                                                                                                                          225 LYKILCGRNEKLYSYVKSLHHPLIEAIPYLHSKAEMNRLYEQATGIMTKPGGVTISECLQ
                                                                                                                                                                                                            RCIPMIFLNPAPGQELENAFYFEEKGFGKIAD----TPEEAIKIVASLTNGNEQL----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
STRAIN-C-125 / JCM 9153;
Takami H., Nakasone K., Takaki Y.;
Tukami H., Nakasone K., Takaki Y.;
Submitted (MAR-2000) to the EMBL/GenBank/DDBJ databases.
EMBL; AP001513; BAB05676.1; -.
SEQUENCE 374 AA; 42361 MW; DA96A0EA33C5AC65 CRC64;
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Last annotation update)
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                    Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;
Actinomycetales; Streptomycineae; Streptomycetaceae; Streptomyces.
NCBI_TaxID=1902;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      235 TVR--LLVDHGYLPVVLCGDNQRLRRTLSG----TPGVLALGWVTDMPGLLHAARALIDN
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Cerdeno A.M., Parkhill J., Barrell B.G., Rajandream M.A.;
Submitted (OCT-2000) to the EMBL/GenBank/DDBJ databases.
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Saunders D.C., Harris D.;
Submitted (OCT-2000) to the EMBL/GenBank/DDBJ databases.
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                                                                                                                                   Last sequence update)
Last annotation update)
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    384
                                                                                                 Created)
    PRT;
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MEDLINE=97000351; PubMed=8843436;
                                                                              01-WAR-2001 (TremBirel. 16, 01-WAR-2001 (TremBirel. 16, 01-WAR-2001 (TremBirel. 16, PUTATIVE SECRETED PROTEIN.
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PRELIMINARY;
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ID Q9S519
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STRAIN—STOKE W, M92;
MEDLINE—S98449815; PubMed—9774562;
MEDLINE—98449815; PubMed—9774562;
MEDLINE—98449815; PubMed—9774562;
"Sequencing of Escherichia coli Olli O-antigen gene cluster and identification of Olli-specific genes.";
I. Clin. Microbiol. 36:3182-3187(1998).
EMBL: AFO'80736; AAD46732.1;
InterPro; IPRO01296;
-..
From From Strong—1: 1.
Transferase.
SEQUENCE 374 AA; 42192 MW; 54COCIEFBBF76B53 CRC64;
                              Escherichia coli.
Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
Escherichia.
                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
STRAIN-STOKE W, M92;
MEDLINE-STOKE W, M92;
MEDLINE-STOKE W, M92;
MEDLINE-STOKE W, M92;
MESTIN D.A., Receves P.R.;
"Sequence and analysis of the O antigen gene (rfb) cluster of Escherichia coli 0111.";
Gene 164:17-23(1995).
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Best Local Similarity 20.9%
Matches 84; Conservative
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Search completed: June 29, 2001, 09:05:04 Job time: 321 sec

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Sequence 6, Appli
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: Application US/08751474

Sequence 2, Application US/08751474

Sequence 2, Application US/08751474

Patent No. S82135

APPLICANT: Hoskins, Joann

APPLICANT: Hoskins, Joann

APPLICANT: Hoskins, Joann

APPLICANT: Statrud, Paul L.

TITLE OF INVENTION: Biosynthetic Gene murG From TITLE OF INVENTION: Streptococcus Pneumoniae

NUMBER OF SEQUENCES: 3

CORRESPONDENCE ADDRESS:

ADDRESSEE: Lilly Corporate Center

CITY: Indianapolis

STATE: Indianapolis

COUNTRY: U.S.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ZIP: 46285

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/751,474
US-08-297-510-6
US-08-479-532-6
US-08-455-526-6
US-08-455-525-6
US-09-139-491-6
US-09-0139-491-6
US-08-867-941-20
US-08-942-0128-25
US-08-942-0128-25
US-08-942-0128-25
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US-07-908-245-2
US-08-514-975B-2
PCT-US95-12507-2
US-08-532-547-9
US-09-019-809-9
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FILING DATE:
CLASSIFICATION: 536
ATTORNEY/AGENT INFORMATION:
NAME: Webster: Thomas D.
REGISTRATION NUMBER: 39,872
REFERENCE/DOCKET NUMBER: 4-99C
TELECOMMUNICATION INFORMATION:
TELEPHONE: 317-276-3334
INFORMATION FOR SEO ID NO: 2:
SEQUENCE CHRACTERISTICS:
SEQUENCE CHRACTERISTICS:
LENGTH: 352 amino acid
TYPE: amino acid
TYPE: amino acid
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Best Local Similarity 20.4%;
Matches, 79; Conservative 80
  ; MOLECULE TYPE: protein US-08-751-474-2
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/cgn2_6/ptodata/2/iaa/5B_COMB.pep:*
/cgn2_6/ptodata/2/iaa/6A_COMB.pep:*
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/cgn2_6/ptodata/2/iaa/PCTUS_COMB.pep:*
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                                          Compugen Ltd
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US-08-47-176-2
US-08-709-784-1
US-08-766-85
PCT-US92-00282-3
US-08-486-604A-10
US-08-405-496A-10
PCT-US92-00282-5
US-08-451-715A-4
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                      GenCore version 4.5
Copyright (c) 1993 - 2000 Com
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US-08-297-494-6
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Maximum Match 100%
Listing first 45 summaries

    protein search, using sw model

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Gapop 10.0 , Gapext 0.5
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length: 2000000000
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19;

74; Gaps

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208 LQRVKNMLYPLALSYICHTFSAPYASLASELFQREVSVVDLVS--
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PCT-US92-00282-6
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STATE: D
COUNTRY:
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                                                                                                                                         62 KLRR-----YESMQNMLD-VFKVGMGIVQSLFIMLRLRPQTLFSKGGFV 104
                                                   111 TFPTPVMSVLTEQFNINIPVATVMTDYR--LHKNWITPYSTRYYVATKETKQDFIDVGID 168
                                                                                    105 SVP-PVIAARVS----GVPVFIHESDLSMGLANKIAYKFATKMY-STFEQASSLSKVEHV 158
                                                                                                                     169 PSTVKVTGIPIDNKFETPINQKQWLID--NNLDPDKQTILMSAGAFGVSKGFDTMITDIL 226
                                                                                                                                                                                        227 AK-SANAQVVMICGKS--KELKRSLTAKFKLTRMYLILGYTKHMNEWMASSQLMITKPGG 283
                                                                                                                                                                                                                                                        284 ITITEGFA----RCIPMIFLNPAPGQELENAFYFEEKGFGKIADTPEEAIKIVASLTNGN 339
                                                                                                                                                                                                                                                                             Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 534;
                                                                                                                                                                                                                                                                                                                                                                                                                                         GENERAL INFORMATION:
APPLICANT: OWENS, IDA S.
TITLE OF INVENTION: THE GENETIC LOCUS UGT1 AND A MUTATION
TITLE OF INVENTION: THE GENETIC LOCUS UGT1 AND A MUTATION
WHORER OF SEQUENCES: 40
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US92/00282
FILING DATE: 19920110
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20.8%; Pred. No. 0.0079;
tive 54; Mismatches 103;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: SCOTT, WATSON T.
REGISTRATION NUMBER: 26581
REFERENCE/DOCKET NUMBER: 91532-PCT
                                                                                                                                                                                                                                                                                                                                                 E: CUSHMAN DARBY & CUSHMAN 1615 L STREET, N.W.
                                                                                                                                                                                                                                                                                                                            340 EQLINMISTMEQDKIKYATQTICRDLLD 367
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TELEPHONE: 202-861-3000
TELEFAX: 202-822-0944
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MEDIUM TYPE: Floppy disk
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Best Local Similarity 20.88
Matches 60; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE CHARACTERISTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     single
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MOLECULE TYPE: protein
PCT-US92-00282-4
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CLASSIFICATION:
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PCT-US92-00282-4
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      204 TILMSAGAFGY---SKGFDTMITDILAKSANAQVVMICGKSKELKRSLTAKFKLTRMYLI 260
                                                                                                                                                                                                                              347 ANNT-ILVKWLPQNDLLGHPMTRAFITHAGSHGVYESICNGVPMVMM-PLFGDQMDNAKR 404
153 VATKETKODFI---DVGIDPSTVKVTGI-----PIDNKFETPINQKOWLIDNNLDPDKQ 203
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                                                                                                                                                                                             261 LGYTKHMNEWMASSQLM-----ITKPGGITITEGFARCIPMIFLNPAPGQELENAFY
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                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 6, Application PC/TUS9200282
GENERAL INFORMATION:
APPLICANT: OWENS, IDA S.
APPLICANT: RITTER, DEPH K.
TITLE OF INVENTION: THE GENETIC LOCUS UGT1 AND A MUTATION
TITLE OF INVENTION: THEREIN.
NUMBER OF SEQUENCES: 40
CORRESPONDENCE ADDRESS:
ADDRESSEE: CUSHMAN DARBY & CUSHMAN
STREET: 1155 L STREET, N.W.
                                                                                                                                                                                                                                                                                           313 FEEKGFG-----KIADTPEEAIKIVASLINGNEQLINMISIMEQDK 353
                                                                                                                                                                                                                                                                                                                     252 ASVWLFRGDFVMDYPRPIMPNMVFIGGINCANGKPLSQEFEAYIN----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          5.3%; Score 109.5; DB 5; ilarity 20.6%; Pred. No. 0.012; Conservative 69; Mismatches 122;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICATION NUMBER: PCT/US92/00282
FILING DATE: 19920110
CLASSIFICATION: 435
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TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-861-3000
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NAME: SCOTT, WATSON T.
REGISTRATION NUMBER: 2658
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
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TELEFAX: 202-822-0944
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COMPUTER READABLE FORM:
WEDIUM TYPE: Floppy
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Best Local Similarity
Matches 78; Conserva
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20036-5601
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195 TKFSDHMTFPQRLANFIANILENYLYH----CLYSKYEILASDLLKRDVSLPALHQNSLW 250
                                                                                                                                                                                        135 LSFLRENOFDALFTDPAMPCGVILAEYLKLPSIYLFRGFPCSLEHIGQSPSPVSYVPRFY 194
                                                                                                                                                                                                                                                       ---VATVMIDYRLHKNWITPYSTRYYVATKETKQDFIDVGIDPSTVK 173
                                                                                                                                                                                                                                                                                                                                                                                                                                               251 LLRYDPVFEYPRPVMPNMIFIGGINCKKKGNLSQEFEAYVNASGEHGIVVFSLG--SMVS 308
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           --ITKPGGITITEGFARCIPMIFLNPAPGQELENAFYFEEKGFG-----KIADTPEEA 328
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               75 KSFPVPYNLEELRIRYRSFGNNHFAASSPLMAPLREYRNNMIVIDMCFFSCOSLLKDSAT 134
      --YYSRPDKLDKCFYKYYGLNK---L 96
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        224 DILAKSANAQVVMICGKSKELKRSLTAKFKLTRMYLILGYTKHMNEWMASSQLM-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    309 EIPEKKA-MEIAEALGR---IPQTLLMRYTGTRPSNLAKNT-ILVKWLPQNDLLGHPKAR
                                                                                                                                                                                                                                                                                                                                                                                174 VTGIPIDNKFETPINQKQWLI-----DNNLDPDKQTILMSAGAFGV---SKGFDTMIT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         BNERAL INFORMATION:
APPLICANT: Vogelstein, Bert
APPLICANT: Kincler, Kenneth W.
APPLICANT: Ge la Chappelle, Albert
TITLE OF INVENTION: Mutator Gene and Hereditary
TITLE OF INVENTION: No. 5591826-Polyposis Colorectal Cancer
NUMBER OF SEQUENCES: 16
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OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STREET: 1001 G Street, N.W.
CITY: Washington
STATE: D.C.
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REFERENCE/DOCKET NUMBER: 01107.44900
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202.508.9100
TELEFAX: 202.508.929
TELEFAX: 197430 BMBB 0T
INFORMATION FOR SEQ. ID NO: SEQUENCE CHARACTERISTICS:
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FILING DATE: 01-JUN-1995
CLASSIFICATION: 530
                                                                                                                           INLLIKEKPDLILLTFPTPVMSVLTEOFNI-
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APPLICATION NUMBER: US 08/160295
FILING DATE: 02-DEC-1993
ATTONEZ/AGENT INFORMATION:
NAME: RAGAN, SARAH A.
REGISTRATION NUMBER: 32,141
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   329 IKIVASLTNGNEQLTNMISTMEQDK 353
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 2, Application US/08457176
Patent No. 5591826
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ZIP: 20001
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
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ADDRESSEE: Banner, B
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TOPOLOGY: 11
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                                                                            223 LS-ITPYES---LASELLQREMSLVEVLSHASVWLFRGDFVFDYPRPIMPNAVFIGGINC 278
                                                                                                                                                                                        231 NAQVVMICGKSKELKRSLTAKFKLTRMYLILGYTKHMNEWMASSQLM------ITKPG 282
                                                                                                                                                                                                                                                                                                                                                                                                       283 GITITEGFARCIPMIFLNPAPGQELENAFYFEEKGFG-----KIADTPEEAIKIVASL 335
                                                                                                                                                                                                                                                                                                                                                                                                                                                   -GIDPSTVKVTGI-- 177
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             9 LIITGS-FGNGHMQVTQSIVNQLNDMNL-DHLSVIEHDLFM---EAHPILTSICKKWYIN 63
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  |::|| |::| | |::| | |:|| |:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| 
                                                                                                                                                                                                                                                                                                                   178 ----PIDNKFETPINQKQWLIDNNLDPDKQTILMSAGAFGV---SKGFDTMITDILAKSA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Indels 115;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 7, Application PC/TUS9200282
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: OWENS, IDA S.
APPLICANT: WITTER, JOSEPH K.
TITLE OF INVENTION: THE GENETIC LOCUS UGT1 AND A MUTATION
TITLE OF INVENTION: THEREIN.
NUMBER OF SEQUENCES: 40
CORRESPONDENCE ADDRESS:
ADDRESSEE: CESHMAN DARBY & CUSHMAN
STREET: 1615 L. STREET, N.W.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US92/00282
FILING DATE: 19920110
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match 5.1%; Score 104.5; DB 5; Best Local Similarity 18.4%; Pred. No. 0.04; Matches 82; Mismatches 166;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ATTORNEY/AGENT INFORMATION:
NAME: SCOTT, WATSON T.
REGISTRATION NUMBER: 26581
REPERCE/DOCKET NUMBER: 91532-PCT
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-861-3000
                          141 KNWITPYSTRYYVATK--ETKQDFIDV---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPOTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TELEX: 6714627 CUSH
INFORMATION FOR SEQ ID NO: 7:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               432 KSYKENIMR-LSSLHKDR 448
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      336 TNGNEQLTNMISTMEQDK 353
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LENGTH: 529 amino acids
                                                                                                                                                                                                            279 VIKKPLSQEFEAYVN-----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       OPERATING SYSTEM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CITY: WASHINGTON
STATE: D.C.
COUNTRY: U.S.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AMINO ACID
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AY: U.S.A.
20036-5601
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CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RESULT 4
PCT-US92-00282-7
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539 FSTVDIQKNGVKFTNS----KLTS--LNEEYTKNKTEYEEAQDAIVKEI--VNISSGXV 589
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            117 MSVLTE--QFNINIPVATVMTDYRLHKNWITPYSTRYYVATKETKQDFIDVGIDPSTVKV 174
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    232 AQVVMICGKSKELKRSLTAKFKLTRMYLILGYTKHMNEWMASSQLMITKPGGITITEGFA 291
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ------HDLFMEAHPILTSICKKWYI 62
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      175 TGI--PIDNKFE-TPINQKQWLIDNNLDPDKQTILMSAGAFGVSKGFDTMITDILAKSAN
                                                                                                                                                                                                                                                                                                                                                                                                                       93;
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TITLE OF INVENTION: Antibody Detection of Mismatch Repair
TITLE OF INVENTION: Protein
NUMBER OF SEQUENCES: 3
CORRESPONDENCE ADDRESS:
ADDRESSEE: ADDRESSE: ADDRESSE: ADDRESSE: ADDRESSE: STREET: 1001 G Street, N.W.
                                                                                                                                                                                                                                                                                                                                                                      Query Match 5.0%; Score 102.5; DB 1; Length 9 Best Local Similarity 22.3%; Pred. No. 0.15; Matches 77; Conservative 45; Mismatches 131; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               292 RCIPMIFLNPAPGQELENAFYFE-------EKGFGKI 321
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        441 TDLRSDFSKFQEMIETTLDMDQVENHEFLVKP-------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        18 GHMQVTQSIVNQLNDMNL--DHLSVIE---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/480,351
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 US-08-709-784-1; Sequence 1, Application US/08709784; Patent No. 6048701
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
                                                                                          LENGTH: 934 amino acids
                                                                                                                                                                                                                                                                                ; ORGANISM: Homo sapiens US-08-457-175-2
                   TELEX: 197430 BBMB UT INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
202.508.9299
                                                                                                                   TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                   MOLECULE TYPE: protein HYPOTHETICAL: YES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICATION NUMBER:
                                                                                                                                                             TOPOLOGY: linear
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APPLICANT: The Joi
                                                                                                                                                                                                                                                          ORIGINAL SOURCE:
                                                                                                                                                                                                           HYPOTHETICAL: Y
ANTI-SENSE: NO
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TELEFAX:
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                                                                                                                                                                                                                                                                                                                                                                              63 NSFKYFRNMYKGFYYSRPDKLDKCFYKYYGLNKLINLL-IKEKPD-----LILLTFPTPV 116
                                                                                                                                                                                                                                                                                                                                                                                                                       ------FQRQAANLQDCYRLYQGINQLPNVIQALEKHEGKHQKLLLAVFVTPL 440
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           117 MSVLTE--QFNINIPVATVMTDYRLHKNWITPYSTRYYVATKETKQDFIDVGIDPSTVKV 174
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 232 AQVVMICGKSKELKRSLTAKFKLTRMYLILGYTKHMNEWNASSQLMITKPGGITITEGFA 291
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             539 FSTVDIQKNGVKFTNS----KLTS--LNEEYTKNKTEYEEAQDAIVKEI--VNISSGYV 589
                                                                                                                                                                                                                                                                                                                               338 GORLVNQWIKQPIADKNRIEERLNLVEAFVEDAELRQTLQEDL-LRRFPDLNRLAKK--- 393
                                                                                                                                                                                                                                                                                18 GHMQVTQSIVNQLNDMNL--DHLSVIE------HDLFWEAHPILTSICKKWYI 62
                                                                                                                                                                                        Length 934;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: Vogelstein, Bert
APPLICANT: Kinzler, Kenneth W.
APPLICANT: de la Chappelle, Albert
TITLE OF INVENTION: Mutator Gene and Hereditary
TITLE OF INVENTION: No. 56934710-Polyposis Colorectal Cancer
NUMBER OF SEQUENCES: 16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              590 E--PMQTLNDVLAQ-LDAVVSFAHVSNGAPVPYVRPAILEKGQGRI 632
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COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
FILING DATE: 01-JUN-1995
CLASSIFICATION: 435
                                                                                                                                                                                        5.0%; Score 102.5; DB 1;
22.3%; Pred. No. 0.15;
tive 45; Mismatches 131;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STREET: Banner, Birch, McKie, and Beckett STREET: 1001 G Street, N.W. CITY: Washington STATE: D.C. COUNTRY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       441 TDLRSDFSKFQEMIETTLDMDQVENHEELVKP-----
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APPLICATION NUMBER: US 08/160295
FILING DATE: 02-DEC-1993
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 2, Application US/08457175 Patent No. 5693470
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REGISTRATION NUMBER: 32,141
REFERENCE/DOCKET UNBER: 01
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202,508,9100
                                                                                                                                                                                                                                      77; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
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CORRESPONDENCE ADDRESS:
ADDRESSEE: Banner, B
                                                                                                                                                                                                                   Similarity
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                                                 ANTI-SENSE: NO
ORIGINAL SOURCE:
ORGANISM: HOM
                        HYPOTHETICAL:
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US-08-457-175-2
                                                                                                    ; ORGANISM
US-08-457-176-2
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                                                                                                                              75 LEGLKPILABEKPDVVLVHGDTTTTLATSLAAFYQRIPVGHVEAGLRTGDLYSPWPEEAN 134
                                                                                                                                                                                    144 --ITPYSTRYYVATKET-KODFIDVGIDPSTVKVTGIPIDNKFETPINGKOWLIDN---- 196
                                                                                                                                                                                                             -----ILDILAKSANAQVVMIC 238
                                                                                                                                                                                                                                                                                                                DKLRSELAANYPFIDPDKKMILVTGHRRESFG-~RGFEEICHALADIATTHQDIQIVYPV 245
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                126 GCSHLLHNKELMASLAESSFD---VMLTDPFLPCSPIVAQ-----YLSLPTVF----F 171
                                                               Gaps
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                                                                                                                                                                                                                                                                                                                                                                                    246 HLNPNVREPVNR-----ILGHVKNVILIDPQEYLPFVWLMNHAWLILTDSGGI 293
                                                                                                                                                                                                                                                                                                                                                         239 GKSKELKRSLTAKFKLTRMYLILGYTKHM----NEW-----MASSQLMITKPGGI 284
                                                            63;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Indels 103;
                                                                                                   93 LNKLINLLIKEKPDLILL-TFPTPVMSVLTEQFNINIPVATVMTDYR---LHKNW--
                  Length 376;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 533;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 3, Application PC/TUS9200282
GENERAL INFORMATION:
APPLICANT: OWENS, IDA S.
APPLICANT: RITTER, JOSEPH K.
TITLE OF INVENTION: THE GENETIC LOCUS UGT1 AND A MUTATION
TITLE OF INVENTION: THEREIN.
                                                            Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CURRENT APPLICATION #1.25
CURRENT APPLICATION DAYS:
FILING DATE: 19920110
CLASSIFICATION: 415
TORNEY/AGENTON: 415
TORNEY/AGENTON: 415
Query Match
4.9%; Score 99.5; DB 5;
Best Local Similarity 19.3%; Pred. No. 0.13;
Matches 74; Conservative 74; Mismatches 132;
                                                            42; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CUSHMAN DARBY & CUSHMAN 15 L STREET, N.W.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COUNTRY: U.S.A.
ZIP: 20036-5601
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ATTORNEY/AGENT INFORMATION:
NAME: SCOTT, WATSON T.
REGISTRATION NUMBER: 26581
REFRENCE/DOCKET NUMBER: 915:
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-861-3000
                  5.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TELEX: 6/714627 CUSH
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
           Ouery Match 5.0%
Best Local Similarity 22.4%
Matches 53; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LENGTH: 533 amino acids
TYPE: AMINO ACID
STRANDEDNESS: single
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MOLECULE TYPE: protein
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CORRESPONDENCE ADDRESS:
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CITY: WASHINGTON
STATE: D.C.
COUNTRY: U.S.A.
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Setting Particant: Lam, Joseph S.

APPLICANT: Lam, Joseph S.

APPLICANT: Burrows, Lori

APPLICANT: Charter. Deborah

APPLICANT: Charter. Deborah

APPLICANT: Charter. Deborah

TITLE OF INVENTION: of O-Antigen in Pseudomonas Aeruginosa

FILE REFERENCE: 6580-089

CURRENT APPLICATION NUMBER: US/08/846,762A

CURRENT FILING DATE: 1997-04-30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            17;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 394 ------FQRQAANLQDCYRLYQGINQLPNVIQALEKHEGKHQKLLLAVFVTPL 440
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      63 NSFKYFRNMYKGFYYSRPDKLDKCFYKYYGLNKLINLL-IKEKPD-----LILLTFPTPV 116
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         117 MSVLTE--QFNINIPVATVMTDYRLHKNWITPYSTRYYVATKETKQDFIDVGIDPSTVKV 174
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           175 TGI--PIDNKFE-TPINQKQWLIDNNLDPDKQTILMSAGAFGVSKGFDTMITDILAKSAN 231
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            232 AQVVMICGKSKELKRSLTAKFKLTRMYLILGYTKHMNEWMASSQLMITKPGGITITEGFA 291
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         539 FSTVDIQKNGVKFTNS-----KLTS--LNEFYTRNKTEYEEAQDAIVKEI--VNISSGYV 589
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ---SFDPNLSEL 481
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            93;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 934;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      590 E--PMQTLNDVLAQ-LDAVVSFAHVSNGAPVPYVRPAILEKGQGRI 632
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                292 RCIPMIFLNPAPGQELENAFYFE--------EKGFGKI 321
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DB 3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          45; Mismatches 131;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                        5.0%; Score 102.5; 22.3%; Pred. No. 0.1
                                                                            1107.57434
                                                                   REFERENCE/DOCKET NUMBER: 1107
TELECOMMUNICATION INFORMATION:
TELEFAN: 202-508-9100
TELEFAN: 202-508-929
INPORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ; ORGANISM: Pseudomonas aeruginosa<sup>7</sup>
US-08-846-762-85
                               NAME: Kagan, Sarah A.
REGISTRATION NUMBER: 32,141
             ATTORNEY/AGENT INFORMATION:
NAME: Kagan, Sarah A.
                                                                                                                                                                                                    : 934 amino acids
amino acid
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SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 85
LENGTH: 376
                                                                                                                                                                                                                                                                                                                                ; ANTI-SENSE: NO
; ORGINAL SOURCE:
; ORGANISM: HOMO sapiens
US-08-709-784-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Local Similarity 22.3 nes 77; Conservative
                                                                                                                                                                                                                                          STRANDEDNESS: Single
TOPOLOGY: linear
MOLECULE TYPE: protein
HYPOTHETICAL: YES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
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Matches
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                                                                                                                                                                                              ---ASGEHGIVVFSLG--SMVSEI 314
                                                                                                                                                                                                                                         ITKPGGITITEGFARCIPMIFLNPAPGQELENAFYFEEKGFG-----KIADTPEEAIK 330
----FRSDFVKDYPRPIMPNMVFV 275
                                              SVLTEQFNINIPVATVMTDYRLHKNWITPYSTRYYVATKETKQDFI---DVGIDPSTVKV
                                                                                                            TGI-----SKGFDTMIDDNKPETPINOKOWLIDNNLDPDKQTILMSAGAFGV---SKGFDTMITDI
                                                                                                                                                                            LAKSANAQVVMICGKSKELKRSLTAKFKLTRMYLILGYTKHMNEWMASSQLM-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: KINK, JOHN A.
APPLICANT: THALLEY, BRUCE S.
APPLICANT: THALLEY, BRUCE S.
APPLICANT: FIRCA, JOSEPH R.
APPLICANT: STAFFORD, DOUGLAS C.
TITLE OF INVENTION: PREVENTION OF C. DIFFICILE DISEASE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER READBLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           E: MEDLEN & CARROLL, LLP
220 MONTGOMERY STREET, SUITE 2200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICATION NUMBER: US/08/480,604A FILING DATE: 07-JUN-1995 CLASSIFICATION: 424
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PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/405,496
FILING DATE: 16-MAR-100E
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/429,791
FILING DATE: 31-0CT-1989
ATORNEY/AGENT INFORMATION:
NAME: INGOLIA, DIANE E.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      UMBER: US 08/161,907
02-DEC-1993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                UMBER: US 08/329,154
25-OCT-1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           UNITED STATES OF AMERICA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              US 07/985,321
                                                                            232 TLASEFLOREVTVODLLSSASV---WL---
                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 10, Application US/08480604A Patent No. 5736139 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                         331 IVASLINGNEQLINMISTMEQDK 353
                                                                                                                                                                                                                                                                                                                                     429 AVINDKSYKENIMR-LSSLHKDR 450
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                                                                                                                                        276 GGINCLHQNPLSQEFEAYIN--
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APPLICATION NUMBER: U
FILING DATE: 25-OCT-1
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APPLICATION NUMBER: C
FILING DATE: 04-DEC-1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FILING DATE:
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US-08-480-604A-10
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1428 LISGELKILMINSNHIQQK--IDYIGFNSELQKNIPYSFVDSEGK-----ENGFINGS 1478
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                                                                                                                                                                                                                                                                                                                                                                                                                                                              ----LLIKEKPDLILLTFPTPVMSVLTEQ-----FNINIPVATVMTDYRLHKNWITPY 147
                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                   2 VTQNKKIL------IITGSFGNGHMQVTQSIVNQLNDMNLDHLSVIEHDLFMEAHPI 52
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    288 -EGFARCIPMIFLNP-----APGQELENAF-----YFEEKGFGKIADTPEEA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      148 STRYYVATKETKQDFIDVGI-----DPSTVKVTGIPIDNKFETPINQKQWLIDNNLDPDK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               203 QTILMSAGAFGVSKGFDTMITDILAKSANAQVVMICGKSKELKRSLTAKFKLT-----
                                                                                                                                                                                                                                                                                                                                                                                   Indels 155;
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                                                                                                                                                                                                                                                                                                                                    Length 2366;
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                        20.0%; Pred. No. 1./,
tive 73; Mismatches 129;
                                                                                                                                                                                                                                                                                                                                    4.8%; Score 98.5; DB 1; 20.0%; Pred. No. 1.7;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 220 MONTGOMERY STREET, SUITE 2200
                   REFERENCE/DOCKET NUMBER: OPHD-01763 TELECOMMUNICATION INFORMATION: TELEPHONE: (415) 705-8410 TELEFAX: (415) 397-8338 INFORMATION FOR SEQ ID NO: 10:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1738 IRYVWS-NDGNDFI--LMSTSEENKV 1760
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CORRESPONDENCE ADDRESS:
ADDRESSEE: MEDLEN & CARROLL, LLP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     329 IKIVASLINGNEQLINMISTMEQDKI 354
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GENERAL INFORMATION:
APPLICANT: WILLIAMS, JAMES A.
TITLE OF INVENTION: VACCINE FOR CI
  40,027
                                                                                                                                                                   2366 amino acids
                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity 20.0°
Matches 89; Conservative
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                                                                                                                                             SEQUENCE CHARACTERISTICS
                                                                                                                                                                                                             TOPOLOGY: linear
MOLECULE TYPE: protein
REGISTRATION NUMBER:
                                                                                                                                                                                            amino acid
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                                                                                                                                                                 LENGTH:
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70 NMYKGFYYSRPDKLDKCF-----YKYYGLNKLINLLIKEKPDLILLTF---PTP 115
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         189 VSYIPRCYTKFSDHMTFSQRVANFLV-----NLLEPYLFYCLFSKYEKLASAVLKRD-V 241
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DVGIDPSTVKVTGIPIDNKFETP-----INQKQWLIDNNLDPDKQTILMSAGA 211
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            269 EWMASSQLM-----ITKPGGITITEGFARCIPMIFLNPAPGQELENAFYFEEKGFG- 319
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Best Local Similarity 21.2%; Pred. No. 0.58;
Matches 85; Conservative 64; Mismatches 147; Indels 104; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  14 SFGNGHMO----VTQSIVNOLNDMNLDHLSVIEHDLFMEAHPILTSICKKWYINSFKYFR 69
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      212 FGV---SKGFDTMITDILAKSANAQVVMICGKSKELKRSLTAKFKLTRMYLILGYTKHMN
                  THE GENETIC LOCUS UGT1 AND A MUTATION THEREIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                           SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCI/US92/00282
FILING DATE: 19920110
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       320 ----KIADTPEEAIKIVASLTNGNEQLTNMISTMEQDK.353
                                                                                 STREET: CUSHMAN DARBY & CUSHMAN STREET: 1615 L STREET, N.W. CITY: WASHINGTON STATE: D.C. COUNTRY
                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER: IBM PC Compatible OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         REFERENCE/DOCKET NUMBER: 91
TELECOMMUNICATION INFORMATION
TELEPHONE: 202-861-3000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                26581
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TELEPHONE: 202-861-3000
TELEFAX: 202-822-0944
TELES: 6/14627 CUSH
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: SCOTT, WATSON T.
REGISTRATION NUMBER: 265
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LENGTH: 531 amino acids TYPE: AMINO ACID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ; TOPOLOGY: linear
; MOLECULE TYPE: protein
PCT-US92-00282-5
                                                                                                                                                                                                                                                           COUNTRY: U.S.A.
ZIP: 20036-5601
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy of
                                                                                                                       CORRESPONDENCE ADDRESS
                               TITLE OF INVENTION:
TITLE OF INVENTION:
NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STRANDEDNESS:
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US-08-451-715A-4
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1428 LISGELKILMLNSNHIQOK -- IDYIGFNGELQKNIPYSFVDSECK -----ENGFINGS 1478
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1527 LTGYYL-----KDDIKISLSLTLQDEKTIKLNSVHLD---ESGVAE------ 1564
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1681 LYGIDSCVNKVVISPNIYTDEINITPVYETNNTYPEVIVLDANYINEKINVNINDL---S 1737
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  288 -EGFARCIPMIFLNP-----APGQELENAF-----YFEEKGFGKIADTPEEA 328
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   2 VTQNKKIL-----IITGSFGNGHMQVTQSIVNQLNDMNLDHLSVIEHDLFMEAHPI 52
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          53 LTS------ICKKWYINSFKYFRNMYKGFYYSRPDKLDKCFYKYYGLNKLIN-- 98
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ----LLIKEKPDLILLTFPTPVMSVLTEQ-----FNINIPVATVMTDYRLHKNWITPY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    203 QTILMSAGAFGVSKGFDTMITDILAKSANAQVVMICGKSKELKRSLTAKFKLT-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match 4.8%; Score 98.5; DB 2; Length 2366; Best Local Similarity 20.0%; Pred. No. 1.7; Matches 89; Conservative 73; Mismatches 129; Indels 155;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ------RMYLILGYTKHMNE--WMASSQLMITKP------GGITIT----
                                                        CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION DATA:
APPLICATION DATA:
FILING DATE: 25-OCT-1994
PRIOR APPLICATION DATA:
APPLICATION DATA:
APPLICATION DATA:
APPLICATION DATA:
FILING DATE: 02-DEC-1993
PRIOR APPLICATION DATA:
APPLICATION DA
APPLICATION NUMBER: US/08/405,496A
FILING DATE: 16-MAR-1995
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PCT-US92-00282-5
Sequence 5, Application PC/TUS9200282
GENERAL INFORMATION:
APPLICANT: OWENS, IDA S.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ; MOLECULE TYPE: protein US-08-405-496A-10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 linear
                               FILING DATE: 16
CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              66
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331 EVPFGQDGDFSKKALIERINANLNNDLGNLLNRLLGMAKKYFNYSLKS 378

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Sequence 4, Application US/08451715A

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TITLE OF INVENTION: Biological Insect Control Agents Expressing
TITLE OF INVENTION: Insect-Specific Toxin Genes, Methods and Compositions
FILE REFERENCE: 28-96a
CURRENT APPLICATION NUMBER: US/08/942,012B
PRIOR APPLICATION NUMBER: 08/729,606
PRIOR APPLICATION NUMBER: 08/729,606
NUMBER OF SEQ ID NOS: 33
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               319 NMLNVFVETFRSIPYRVLWKVDKSDKIFDNIPSNVLIQRWFPQRRVLKHRN-----VKVF 373
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       265 PSNVQYLGGIHIDPAVTSVADE----IDNDLAEFLENSTM--GVVYVSLGSSVRASDMDS 318
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              278 ITKPGGITITEGFARCIPMIFLNPAPGQELENAFYFEEKGFGKIADTPEEAIKIVASLTN 337
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    169 PSTVK-VTGIPIDNKFETPINQKQWLIDNNLDPDKQTILMSAGAFGVSKGFDTMITDILA 227
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            228 KSANA-----QVVWICGKSKELKRSLTAKFKLTRMYLILGYTKHMNEWMASSQLM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               4.4%; Score 91; DB 4; Length 515; 24.0%; Pred. No. 0.87; Live 33; Mismatches 101; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      338 GNEQLINMISTMEQDKIKYATQTI-CRDLLDLIGHSSQPQEIYGKVPLY 385
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    423 DARQLTEIVMDV-ADNEKYKNGTLWLRDAI-----MDQPMRPLEKAVWY 465
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TYPE: PRT . ORGANISM: Spodoptera littoralis nuclear polyhedrosis virus US-08-942-012B-32
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 4, Application US/09005180A

Batent No. 6124446

Batent Involvation

APPLICANT: Hillman, Jennifer L.

APPLICANT: Corley, Neil C.

APPLICANT: Shah, Purvi

TITLE OF INVENTION: HUMAN VPS35/MEM3-RELATED PROTEIN
NUMBER OF SEQUENCES: 4

CORRESPONDENCE ADDRESS:

ADDRESSEE: Incyte Pharmaceuticals, Inc.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM COMPAILIBLE
COMPUTER: IBM COMPAILIBLE
SOFTWARE: FASTSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/005,180A
                                                                                                        ; Sequence 32, Application US/08942012B
; Patent No. 6235278
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PatentIn Ver. 2.0
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CITY: Palo Alto
STATE: CA
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Conservative
                                                                                                                                                                                       Miller, Lois K
                                                                                                                                                                                                                APPLICANT: Lu, Albert
APPLICANT: Dierks, Peter
APPLICANT: Black, Bruce
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Best Local Similarity
Matches 55; Conserv
                                                                                                                                                                 GENERAL INFORMATION: APPLICANT: Miller,
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                                                      RESULT 14
US-08-942-012B-32
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US-09-005-180A-4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQ ID NO 32
LENGTH: 515
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               19;
                                                                                                  APPLICANT: Hounan, Fariba
APPLICANT: Shen, Xiaoyu
APPLICANT: Schimmel, Paul R.
TITLE OF INVENTION: Helicobacter Aminoacyl-tRNA Synthetase
TITLE OF INVENTION: Proteins, Nucleic Acids and Strains Comprising Same
NUMBER OF SEQUENCES: 67
CORRESPONDENCE ADDRESS:
ADDRESSE: Hamilton, Brook, Smith & Reynolds, P.C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            -----LLIKEKPDLILLTFPTPVMSVLTEQFNINIPVATVMTDYRLH 140
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        200 PDKQTILMSAGAFGVSKGFDTMITDILAKSANAQVVMICGK---SKELKRSLTAKFKLTR 256
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 190 KNEVTSF-----IEQGLLDLSITRTSFE-WGIPLPKKMNDPKHVVYVWL---- 232
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            233 ---DALLNYASALGYLNGLD-----NKMAHFECARHIVGKDILRFHAIYWPAFL 278
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MYLILGYTKHM - - NEWMASSQLMITKPGGITITEGFARCIPMIFLNPAPGQELENAFYFE 314
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MSLNLPLFKQLCVHGWWT1EGVKMSKSLGNVLD---AQKLAMEY-----GIEELRYFLLR 330
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          82 ----DFFNLDYDGFIRTTDSEHQKCVQNAFEIMFEKGDIYKGAYSGYYCVSCESYCAISK 137
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match 4.5%; Score 92; DB 1; Length 648;
Best Local Similarity 19.6%; Pred. No. 0.99;
Matches 80; Conservative 58; Mismatches 152; Indels 118; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      62 INSFKYFRNMYKGFYYSRPDKLDKC-----FYK------YGLNK 95
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                4 QNKKILLITGSFGNGHMQVTQS--IVNQLNDMNLDHLSVIEHDLFMEAHPILTSICKKWY 61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               38 QGEEVFFLTGTDEHG-QKIEQSARLRNQSPKAYADSISAIFKD------QW- 81
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA: US/08/451,715A FILING DATE: 26-MAY-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: BFOOK, DAVIG E
REGISTRATION NUMBER: 22,592
REFERENCE/DOCKET NUMBER: CP194
TELEPHONE: 617-861-6240
TELEPHONE: 617-861-5240
INFORMATION FOR SEQ ID NO: 4:
                                                                                                                                                                                                                                                                                                                  STREET: Two Militia Drive CITY: Lexington
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            : 648 amino acids
amino acid
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                                                      Tao, Jianshi
Qui, Yan
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                                                                                                                                                                                                                                                                                                                                                                            Massachusetts
                                GENERAL INFORMATION:
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US-08-451-715A-4
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                                                                                                                                                                                                                                                                                                                                                                                                 COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                            STATE:
Patent No.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  :|| : | | : | | : :|::| | 425 AYKNILALQSIS---LQKKVYNEIIDILMDREVEEMADNDSESKLHPPGHSAYLVIEDKL 481
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     542 MNTTSFKQTMKNKIQFSLEAQLEILLLIKSSFIKGGINVKY--TFPAIITNFWKLMRKCR 599
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        46 FMEAH-PILTSI---CKKWYINSFKYFRNMYKGFYYSRPDKLDKCFYKYYGLNKLINLLI 101
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               482 QVQRLLSICEPLIISRSGPPANVASSDTNVDEVFFNRHDEEESWILDPIQEKLAHLIHWI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match 4.3%; Score 89; DB 4; Length 937; Best Local Similarity 18.0%; Pred. No. 3.5; Matches 72; Conservative 66; Mismatches 125; Indels 136;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     331 SLQQFIPLVESVIVLSLKWYPNNFD------
                                                                                                      ATTORNEY ACENT INFORMATION:
NAME: Billings, Lucy J.
REGISTRATION NUMBER: 36,749
REFERENCE/DOCKET NUMBER: PF-0457 US
TELEPHONE: 650-855-0555
FILING DATE: Filed January 8, 1998
                                                                                                                                                                                                                                                              TELEX:
INFORMATION FOR SEQ ID NO: 4
SEQUENCE CHARACTERISTICS:
LENGTH: 937 amino acid
TYPE: amino acid
                                                                                                                                                                                                                                                TELEFAX: 650-845-4166
                     CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                          single
                                                                                                                                                                                                                                                                                                                                                                                STRANDEDNESS: Sing

TOPOLOGY: linear

TOPOLOGY: linear

IMBDIATE SOURCE:

LIBRARY: GenBank

CLONE: 854543

US-09-005-180A-4
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